

# Sequence Listing

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 Gerritsen, Mary E.  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, J. Christopher  
 Gurney, Austin L.  
 Kljavin, Ivar J.  
 Napier, Mary A.  
 Pan, James  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Watanabe, Colin K.  
 Williams, P. Mickey  
 Wood, William I.  
 Zhang, Zemin

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Ile	Pro	Gly	Leu	Glu	His	Ala	Ser	Ile	Glu	Gly	Pro	Ile	Ala	Asn
				275					280					285
Leu	Ser	Val	Leu	Gly	Thr	Glu	Glu	Leu	Arg	Gln	Arg	Glu	His	Tyr
				290					295					300
Leu	Lys	Gln	Lys	Arg	Asp	Lys	Leu	Met	Ser	Met	Arg	Lys	Asp	Met
				305					310					315
Arg	Thr	Lys	Gln	Ile	Gln	Asn	Met	Glu	Gln	Lys	Gly	Lys	Pro	Thr
				320					325					330
Gly	Glu	Val	Glu	Glu	Met	Thr	Glu	Lys	Pro	Glu	Met	Thr	Ala	Glu
				335					340					345
Glu	Lys	Gln	Thr	Leu	Leu	Lys	Arg	Arg	Leu	Leu	Ala	Glu	Lys	Leu
				350					355					360
Lys	Glu	Glu	Val	Ile	Asn	Lys								
				365										

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 <211> 418  
 <212> DNA  
 <213> Homo sapiens

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 aaggttacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150  
 tgcacttctc ctcttgcaaa gaccataca tcacaggcca tttttgcaac 200  
 ctgtgttggc agcagaagat ttactatct ttaaagcaat gatggtccag 250  
 aaaaacattg aaatgcagct gcaagccatt cgaataattc aagagagaaa 300





tcctggaagg aattctctga tttcatgaag tggccattc ctgcctttct 500  
 ttatttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 550  
 cagccatggc tggtatcttc tcaaatttta gcattataac aacagctctt 600  
 ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 650  
 cctcctgact ttatttttgt ctattgtggc cttgactgcc gggactaaaa 700  
 ctttacagca caacttggca ggacgtggat ttcacacga tgcctttttc 750  
 agcccttcca attcctgcct tcttttcaga agtgagtgtc ccagaaaaga 800  
 caattgtaca gcaaaggaat ggacttttcc tgaagctaaa tggaacacca 850  
 cagccagagt tttcagtcac atccgtcttg gcatgggcca tgttcttatt 900  
 atagtccagt gttttatttc ttcaatggct aatatctata atgaaaagat 950  
 actgaaggag gggaaccagc tcaactgaaag catcttcata cagaacagca 1000  
 aactctatatt ctttggcatt ctgtttaatg ggctgactct gggccttcag 1050  
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 tgcattttca gtagccctta tttttgtaac tgcattccag ggcctttcag 1150  
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 caggttacca ctgtcattat cacaacagtg tctgtcctgg tctttgactt 1250  
 caggccctcc ctggaatttt tcttggaagc cccatcagtc cttctctcta 1300  
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 aagcttccaa aaaacttgta ataactatgt tagctatagc ttgtatatac 1800  
 acatagagat caatttgcca aatattcaca atcatgtagt tctagtttac 1850  
 atgccaaagt cttccctttt taacattata aaagctaggt tgtctcttga 1900  
 attttgaggc cctagagata gtcattttgc aagtaaagag caacgggacc 1950  
 ctttctaaaa acgttggttg aaggacctaa atacctggcc ataccataga 2000  
 tttgggatga tgtagtctgt gctaaatatt ttgctgaaga agcagtttct 2050



Ala Met Ala Val	Ile Phe Ser Asn Phe	Ser Ile Ile Thr Thr	Ala
	125	130	135
Leu Leu Phe Arg	Ile Val Leu Lys Arg	Arg Leu Asn Trp Ile	Gln
	140	145	150
Trp Ala Ser Leu	Leu Thr Leu Phe Leu	Ser Ile Val Ala Leu	Thr
	155	160	165
Ala Gly Thr Lys	Thr Leu Gln His Asn	Leu Ala Gly Arg Gly	Phe
	170	175	180
His His Asp Ala	Phe Phe Ser Pro Ser	Asn Ser Cys Leu Leu	Phe
	185	190	195
Arg Ser Glu Cys	Pro Arg Lys Asp Asn	Cys Thr Ala Lys Glu	Trp
	200	205	210
Thr Phe Pro Glu	Ala Lys Trp Asn Thr	Thr Ala Arg Val Phe	Ser
	215	220	225
His Ile Arg Leu	Gly Met Gly His Val	Leu Ile Ile Val Gln	Cys
	230	235	240
Phe Ile Ser Ser	Met Ala Asn Ile Tyr	Asn Glu Lys Ile Leu	Lys
	245	250	255
Glu Gly Asn Gln	Leu Thr Glu Ser Ile	Phe Ile Gln Asn Ser	Lys
	260	265	270
Leu Tyr Phe Phe	Gly Ile Leu Phe Asn	Gly Leu Thr Leu Gly	Leu
	275	280	285
Gln Arg Ser Asn	Arg Asp Gln Ile Lys	Asn Cys Gly Phe Phe	Tyr
	290	295	300
Gly His Ser Ala	Phe Ser Val Ala Leu	Ile Phe Val Thr Ala	Phe
	305	310	315
Gln Gly Leu Ser	Val Ala Phe Ile Leu	Lys Phe Leu Asp Asn	Met
	320	325	330
Phe His Val Leu	Met Ala Gln Val Thr	Thr Val Ile Ile Thr	Thr
	335	340	345
Val Ser Val Leu	Val Phe Asp Phe Arg	Pro Ser Leu Glu Phe	Phe
	350	355	360
Leu Glu Ala Pro	Ser Val Leu Leu Ser	Ile Phe Ile Tyr Asn	Ala
	365	370	375
Ser Lys Pro Gln	Val Pro Glu Tyr Ala	Pro Arg Gln Glu Arg	Ile
	380	385	390
Arg Asp Leu Ser	Gly Asn Leu Trp Glu	Arg Ser Ser Gly Asp	Gly
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Glu Glu Leu Glu	Arg Leu Thr Lys Pro	Lys Ser Asp Glu Ser	Asp
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Glu Asp Thr Phe			

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<211> 755  
<212> DNA  
<213> Homo sapiens

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ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 150  
tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 200  
cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 250  
acagtgcgtg agtcatcctg taatatgctc cttgtcaaca atgtatacat 300  
tcctgctagg tgccatattc attgctttaa gctcaagtcg catcttacta 350  
gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 400  
tgtgaatgtg tgctcagaac tgggtgaagct agttttctgt gtgcttgtgt 450  
cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 500  
tcctggaagg aattctctga tttcatgaag tgggccattc ctgcctttct 550  
ttatttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 600  
cagccatggc tggtatcttc tcaaatttta gcattataac aacagctctt 650  
ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700  
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cttta 755

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
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<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcagagaatt ccttccagga 20

<210> 18  
<211> 40  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgtctgt agtcatcctg taatatgctc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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gcggcctgcg gggcagagga gcatcccgtc taccaggctc caagcggcgt 150  
ggcccgcggg tcatggccaa aggagaaggc gccgagagcg gctccgcggc 200  
ggggctgcta cccaccagca tcttccaaag cactgaacgc ccggcccagg 250  
tgaagaaaga accgaaaaag aagaaacaac agttgtctgt ttgcaacaag 300  
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<210> 20  
<211> 458  
<212> PRT  
<213> Homo sapiens

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Trp Ala Glu Pro Gly Met Pro Ser Gln Thr Pro Trp Trp Ala Ser  
20 25 30  
Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro  
35 40 45  
Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser  
50 55 60  
Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr  
65 70 75  
Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met  
80 85 90  
Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr  
95 100 105

Glu	Arg	Asp	Ser	Ala 110	Thr	Ala	Tyr	Arg	Met 115	Thr	Val	Glu	Val	Leu 120
Gly	Thr	Val	Leu	Gly 125	Thr	Ala	Ile	Gln	Gly 130	Gln	Ile	Val	Gly	Gln 135
Ala	Asp	Thr	Pro	Cys 140	Phe	Gln	Asp	Phe	Asn 145	Ser	Ser	Thr	Val	Ala 150
Ser	Gln	Ser	Ala	Asn 155	His	Thr	His	Gly	Thr 160	Thr	Ser	His	Arg	Glu 165
Thr	Gln	Lys	Ala	Tyr 170	Leu	Leu	Ala	Ala	Gly 175	Val	Ile	Val	Cys	Ile 180
Tyr	Ile	Ile	Cys	Ala 185	Val	Ile	Leu	Ile	Leu 190	Gly	Val	Arg	Glu	Gln 195
Arg	Glu	Pro	Tyr	Glu 200	Ala	Gln	Gln	Ser	Glu 205	Pro	Ile	Ala	Tyr	Phe 210
Arg	Gly	Leu	Arg	Leu 215	Val	Met	Ser	His	Gly 220	Pro	Tyr	Ile	Lys	Leu 225
Ile	Thr	Gly	Phe	Leu 230	Phe	Thr	Ser	Leu	Ala 235	Phe	Met	Leu	Val	Glu 240
Gly	Asn	Phe	Val	Leu 245	Phe	Cys	Thr	Tyr	Thr 250	Leu	Gly	Phe	Arg	Asn 255
Glu	Phe	Gln	Asn	Leu 260	Leu	Leu	Ala	Ile	Met 265	Leu	Ser	Ala	Thr	Leu 270
Thr	Ile	Pro	Ile	Trp 275	Gln	Trp	Phe	Leu	Thr 280	Arg	Phe	Gly	Lys	Lys 285
Thr	Ala	Val	Tyr	Val 290	Gly	Ile	Ser	Ser	Ala 295	Val	Pro	Phe	Leu	Ile 300
Leu	Val	Ala	Leu	Met 305	Glu	Ser	Asn	Leu	Ile 310	Ile	Thr	Tyr	Ala	Val 315
Ala	Val	Ala	Ala	Gly 320	Ile	Ser	Val	Ala	Ala 325	Ala	Phe	Leu	Leu	Pro 330
Trp	Ser	Met	Leu	Pro 335	Asp	Val	Ile	Asp	Asp 340	Phe	His	Leu	Lys	Gln 345
Pro	His	Phe	His	Gly 350	Thr	Glu	Pro	Ile	Phe 355	Phe	Ser	Phe	Tyr	Val 360
Phe	Phe	Thr	Lys	Phe 365	Ala	Ser	Gly	Val	Ser 370	Leu	Gly	Ile	Ser	Thr 375
Leu	Ser	Leu	Asp	Phe 380	Ala	Gly	Tyr	Gln	Thr 385	Arg	Gly	Cys	Ser	Gln 390
Pro	Glu	Arg	Val	Lys 395	Phe	Thr	Leu	Asn	Met 400	Leu	Val	Thr	Met	Ala 405
Pro	Ile	Val	Leu	Ile 410	Leu	Leu	Gly	Leu	Leu 415	Leu	Phe	Lys	Met	Tyr 420

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln  
425 430 435

Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp  
440 445 450

Ser Thr Glu Leu Ala Ser Ile Leu  
455

<210> 21  
<211> 571  
<212> DNA  
<213> Homo sapiens

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accctatgaa gccacgacgt ctgagccaat cgcctacttc cggggcctac 150  
ggctgggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200  
ttcacctcct tggctttcat gctggtggag gggaactttg tcttgttttg 250  
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cggtttgcca agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400  
atctctcatc ttggtggccc tcatggagag taacctcatc attacatatg 450  
cggtagctgt ggcagctggc atcagtgtag cagctgcctt cttactaccc 500  
tggtccatgc tgccatgatg cattgacgac ttccatctga agcagcccca 550  
cttccatgga accgagccca t 571

<210> 22  
<211> 1173  
<212> DNA  
<213> Homo sapiens

<400> 22  
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aaacagaaaa cctgttagaa atgtggtggt ttcagcaagg cctcagtttc 150  
cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200  
cattactgca gtaacactcc accatataga cccggcttta ccttatatca 250  
gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300  
aatattgogg cagttttatg cattgctacc atttatgttc gttataagca 350  
agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400  
ctggccttgt acttgaata ctgagttgtt taggactttc tattgtggca 450





Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Ile	140	145	150
His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val	Ile	Trp	155	160	165
Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val	Leu	170	175	180
His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp	185	190	195
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Val	Leu	His	Met	Ile	Thr	Thr	Ala	200	205	210
Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr	215	220	225
Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn	230	235	240
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	245	250	255
Asn	Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile					260	265	

<210> 24  
 <211> 485  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 14, 484  
 <223> unknown base

<400> 24  
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 ctgatgccga gttccgtctc tcgggtcttt tcttggtccc aggcaaagcg 100  
 gagcggagat cctcaaacgg cctagtgttt cgcgcttccg gagaaaatca 150  
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 aaccctttcc cacaaaagct aattgagtac acgttctctg tgagtacacg 250  
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 attttgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtgggtttca 350  
 gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400  
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 gctttacctt atatcagtga cactggtaca gtanc 485

<210> 25  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 26  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
ggagatagct gctatgggtt cttcaggcac aacttaacat gggaag 46

<210> 27  
<211> 1399  
<212> DNA  
<213> Homo sapiens

<400> 27  
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ctgccccgcg ggccgggggtg cggagccgac atgcgcccgc ttctcggcct 100  
ccttctggtc ttgcgccggt gcaccttcgc cttgtacttg ctgtcgacgc 150  
gactgccccg cgggcggaga ctgggctcca ccgaggaggc tggaggcagg 200  
tcgctgtggt tcccctccga cctggcagag ctgcgggagc tctctgaggt 250  
ccttcgagag taccggaagg agcaccaggc ctacgtgttc ctgctcttct 300  
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ctgaatgttt tagctggtgc cttgtttggg ccatggctgg ggcttctgct 400  
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cggccccaat tctgaacatt cccatcgtgc agttcttctt ctcaattctt 650  
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tgcagtgtct tttcagaaaag gacactctgc tcttgaaggt gtattacatc 1050  
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 agcctggcca agatggtgaa atcctgtctc taataaaaat acaaaaatta 1250  
 gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300  
 gcaggagaat tgcttgaacc aagggtggcag aggttgcagt aagccaagat 1350  
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<210> 28  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
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 Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg  
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 Leu Gly Ser Thr Glu Glu Ala Gly Gly Arg Ser Leu Trp Phe Pro  
 35 40 45  
 Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu  
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 Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly  
 65 70 75  
 Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe  
 80 85 90  
 Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu  
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 Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr  
 110 115 120  
 Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe  
 125 130 135  
 Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg  
 140 145 150  
 Asn Ser Leu Phe Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met  
 155 160 165  
 Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile  
 170 175 180  
 Pro Ile Val Gln Phe Phe Phe Ser Val Leu Ile Gly Leu Ile Pro  
 185 190 195  
 Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu  
 200 205 210

Thr Ser Leu Asp Ala Leu Phe Ser Trp Asp Thr Val Phe Lys Leu  
 215 220 225  
 Leu Ala Ile Ala Met Val Ala Leu Ile Pro Gly Thr Leu Ile Lys  
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 245 250 255  
 Asn His Ile His Ser Arg Lys Asp Thr  
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 <212> DNA  
 <213> Homo sapiens

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 ggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150  
 tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200  
 tcagagactg ttgatttggg gagacagacc ggccatcagt gtggcatgtc 250  
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 ctgagagacc cccccgcgag tatcctctcc ttatagttgt gtataagggt 350  
 ctogcaacct tgggattaat ctgctcact gcctactttg tgattcaacc 400  
 ttccagccca ttagcacctg agccagtgtt ttctggagct cacacctggc 450  
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 tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550  
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 <212> PRT  
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 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val  
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 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala  
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 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val  
 80 85 90  
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 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu  
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 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys  
 155 160 165  
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His  
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 185 190 195  
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser  
 200 205 210  
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp  
 215 220 225  
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln  
 230 235 240  
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro  
 245 250 255

Lys	Asp	Ala	Ser	Leu	Asn	Lys	Cys	Ser	Phe	Leu	His	Pro	Glu	Pro	
				260					265					270	
Val	Val	Gly	Ser	Lys	Met	His	Lys	Met	Pro	Asp	Leu	Phe	Ile	Ile	
				275					280					285	
Gly	Ser	Gly	Glu	Ala	Met	Leu	Gln	Leu	Ile	Pro	Pro	Phe	Gln	Cys	
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Arg	Arg	His	Cys	Gln	Ser	Val	Ala	Met	Pro	Ile	Glu	Pro	Gly	Asp	
				305					310					315	
Ile	Gly	Tyr	Val	Asp	Thr	Thr	His	Trp	Lys	Val	Tyr	Val	Ile	Ala	
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Arg	Gly	Val	Gln	Pro	Leu	Val	Ile	Cys	Asp	Gly	Thr	Ala	Phe	Ser	
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 gcagagcgct gctcctggct ggtgccactg gtgcgcacgc tgctagaccg 150  
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Gly	Thr	Thr	Pro	Val	Ser	Ser	Pro	Ser	Gln	Thr	Pro	Arg	Pro	Gln	
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Pro	Gly	Pro	Ile	Pro	Pro	His	Thr	Gln	Val	Arg	Asn	Gln	Val	Tyr	
				305					310					315	
Ser	Trp	Leu	Leu	Arg	Leu	Arg	Pro	Pro	Ser	Gln	Gly	Tyr	Leu	Ser	
				320					325					330	
Ser	Arg	Ser	Pro	Gln	Glu	Met	Leu	Arg	Ala	Ser	Gly	Leu	Thr	Gln	
				335					340					345	
Lys	Trp	Val	Gln	Arg	Glu	Ile	Ser	Asn	Phe	Glu	Tyr	Leu	Met	Gln	
				350					355					360	
Leu	Asn	Thr	Ile	Ala	Gly	Arg	Thr	Tyr	Asn	Asp	Leu	Ser	Gln	Tyr	
				365					370					375	
Pro	Val	Phe	Pro	Trp	Val	Leu	Gln	Asp	Tyr	Val	Ser	Pro	Thr	Leu	
				380					385					390	
Asp	Leu	Ser	Asn	Pro	Ala	Val	Phe	Arg	Asp	Leu	Ser	Lys	Pro	Ile	
				395					400					405	
Gly	Val	Val	Asn	Pro	Lys	His	Ala	Gln	Leu	Val	Arg	Glu	Lys	Tyr	
				410					415					420	
Glu	Ser	Phe	Glu	Asp	Pro	Ala	Gly	Thr	Ile	Asp	Lys	Phe	His	Tyr	
				425					430					435	
Gly	Thr	His	Tyr	Ser	Asn	Ala	Ala	Gly	Val	Met	His	Tyr	Leu	Ile	
				440					445					450	
Arg	Val	Glu	Pro	Phe	Thr	Ser	Leu	His	Val	Gln	Leu	Gln	Ser	Gly	
				455					460					465	
Arg	Phe	Asp	Cys	Ser	Asp	Arg	Gln	Phe	His	Ser	Val	Ala	Ala	Ala	
				470					475					480	
Trp	Gln	Ala	Arg	Leu	Glu	Ser	Pro	Ala	Asp	Val	Lys	Glu	Leu	Ile	
				485					490					495	
Pro	Glu	Phe	Phe	Tyr	Phe	Pro	Asp	Phe	Leu	Glu	Asn	Gln	Asn	Gly	
				500					505					510	
Phe	Asp	Leu	Gly	Cys	Leu	Gln	Leu	Thr	Asn	Glu	Lys	Val	Gly	Asp	
				515					520					525	
Val	Val	Leu	Pro	Pro	Trp	Ala	Ser	Ser	Pro	Glu	Asp	Phe	Ile	Gln	
				530					535					540	
Gln	His	Arg	Gln	Ala	Leu	Glu	Ser	Glu	Tyr	Val	Ser	Ala	His	Leu	
				545					550					555	
His	Glu	Trp	Ile	Asp	Leu	Ile	Phe	Gly	Tyr	Lys	Gln	Arg	Gly	Pro	
				560					565					570	
Ala	Ala	Glu	Glu	Ala	Leu	Asn	Val	Phe	Tyr	Tyr	Cys	Thr	Tyr	Glu	
				575					580					585	

Gly	Ala	Val	Asp	Leu 590	Asp	His	Val	Thr	Asp 595	Glu	Arg	Glu	Arg	Lys 600
Ala	Leu	Glu	Gly	Ile 605	Ile	Ser	Asn	Phe	Gly 610	Gln	Thr	Pro	Cys	Gln 615
Leu	Leu	Lys	Glu	Pro 620	His	Pro	Thr	Arg	Leu 625	Ser	Ala	Glu	Glu	Ala 630
Ala	His	Arg	Leu	Ala 635	Arg	Leu	Asp	Thr	Asn 640	Ser	Pro	Ser	Ile	Phe 645
Gln	His	Leu	Asp	Glu 650	Leu	Lys	Ala	Phe	Phe 655	Ala	Glu	Val	Thr	Val 660
Ser	Ala	Ser	Gly	Leu 665	Leu	Gly	Thr	His	Ser 670	Trp	Leu	Pro	Tyr	Asp 675
Arg	Asn	Ile	Ser	Asn 680	Tyr	Phe	Ser	Phe	Ser 685	Lys	Asp	Pro	Thr	Met 690
Gly	Ser	His	Lys	Thr 695	Gln	Arg	Leu	Leu	Ser 700	Gly	Pro	Trp	Val	Pro 705
Gly	Ser	Gly	Val	Ser 710	Gly	Gln	Ala	Leu	Ala 715	Val	Ala	Pro	Asp	Gly 720
Lys	Leu	Leu	Phe	Ser 725	Gly	Gly	His	Trp	Asp 730	Gly	Ser	Leu	Arg	Val 735
Thr	Ala	Leu	Pro	Arg 740	Gly	Lys	Leu	Leu	Ser 745	Gln	Leu	Ser	Cys	His 750
Leu	Asp	Val	Val	Thr 755	Cys	Leu	Ala	Leu	Asp 760	Thr	Cys	Gly	Ile	Tyr 765
Leu	Ile	Ser	Gly	Ser 770	Arg	Asp	Thr	Thr	Cys 775	Met	Val	Trp	Arg	Leu 780
Leu	His	Gln	Gly	Gly 785	Leu	Ser	Val	Gly	Leu 790	Ala	Pro	Lys	Pro	Val 795
Gln	Val	Leu	Tyr	Gly 800	His	Gly	Ala	Ala	Val 805	Ser	Cys	Val	Ala	Ile 810
Ser	Thr	Glu	Leu	Asp 815	Met	Ala	Val	Ser	Gly 820	Ser	Glu	Asp	Gly	Thr 825
Val	Ile	Ile	His	Thr 830	Val	Arg	Arg	Gly	Gln 835	Phe	Val	Ala	Ala	Leu 840
Arg	Pro	Leu	Gly	Ala 845	Thr	Phe	Pro	Gly	Pro 850	Ile	Phe	His	Leu	Ala 855
Leu	Gly	Ser	Glu	Gly 860	Gln	Ile	Val	Val	Gln 865	Ser	Ser	Ala	Trp	Glu 870
Arg	Pro	Gly	Ala	Gln 875	Val	Thr	Tyr	Ser	Leu 880	His	Leu	Tyr	Ser	Val 885
Asn	Gly	Lys	Leu	Arg 890	Ala	Ser	Leu	Pro	Leu 895	Ala	Glu	Gln	Pro	Thr 900

Ala Leu Thr Val Thr Glu Asp Phe Val Leu Leu Gly Thr Ala Gln  
905 910 915

Cys Ala Leu His Ile Leu Gln Leu Asn Thr Leu Leu Pro Ala Ala  
920 925 930

Pro Pro Leu Pro Met Lys Val Ala Ile Arg Ser Val Ala Val Thr  
935 940 945

Lys Glu Arg Ser His Val Leu Val Gly Leu Glu Asp Gly Lys Leu  
950 955 960

Ile Val Val Val Ala Gly Gln Pro Ser Glu Val Arg Ser Ser Gln  
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Phe Ala Arg Lys Leu Trp Arg Ser Ser Arg Arg Ile Ser Gln Val  
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<210> 35  
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<212> DNA  
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Cys	Phe	Lys	Cys	Cys 155	Leu	Trp	Cys	Leu	Glu 160	Lys	Phe	Ile	Lys	Phe 165
Leu	Asn	Arg	Asn	Ala 170	Tyr	Ile	Met	Ile	Ala 175	Ile	Tyr	Gly	Lys	Asn 180
Phe	Cys	Val	Ser	Ala 185	Lys	Asn	Ala	Phe	Met 190	Leu	Leu	Met	Arg	Asn 195
Ile	Val	Arg	Val	Val 200	Val	Leu	Asp	Lys	Val 205	Thr	Asp	Leu	Leu	Leu 210
Phe	Phe	Gly	Lys	Leu 215	Leu	Val	Val	Gly	Gly 220	Val	Gly	Val	Leu	Ser 225
Phe	Phe	Phe	Phe	Ser 230	Gly	Arg	Ile	Pro	Gly 235	Leu	Gly	Lys	Asp	Phe 240
Lys	Ser	Pro	His	Leu 245	Asn	Tyr	Tyr	Trp	Leu 250	Pro	Ile	Met	Thr	Ser 255
Ile	Leu	Gly	Ala	Tyr 260	Val	Ile	Ala	Ser	Gly 265	Phe	Phe	Ser	Val	Phe 270
Gly	Met	Cys	Val	Asp 275	Thr	Leu	Phe	Leu	Cys 280	Phe	Leu	Glu	Asp	Leu 285
Glu	Arg	Asn	Asn	Gly 290	Ser	Leu	Asp	Arg	Pro 295	Tyr	Tyr	Met	Ser	Lys 300
Ser	Leu	Leu	Lys	Ile 305	Leu	Gly	Lys	Lys	Asn 310	Glu	Ala	Pro	Pro	Asp 315
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<213> Artificial Sequence
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Phe	Ser	Ile	His	Phe	Gly	Phe	Lys	His	Lys	Phe	Leu	Ala	Ser	Asp	
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Val	Val	Phe	Ala	Thr	Met	Ser	Leu	Met	Glu	Ser	Pro	Glu	Lys	Asp	
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Gly	Ser	Gly	Thr	Asp	His	Phe	Ile	Gln	Ala	Leu	Asp	Ser	Leu	Ser	
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His	Phe	Asp	Leu	Ser	Val	Ile	Glu	Leu	Lys	Ala	Glu	Asp	Arg	Ser	
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<210> 46

<211> 3089  
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<211> 673

<212> PRT

<213> Homo sapiens

<400> 52

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Ser	Gln	Pro	Gln	Thr	Val	Phe	Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr
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Val	Pro	Arg	Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Val	Phe
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Pro	Gly	Leu	Gln	Leu	Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Ala	Ser
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Arg	Pro	Glu	Asp	Leu 260	Ala	Gly	Leu	Ala	Ala 265	Leu	Gln	Glu	Leu	Asp 270
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Ser	His	Val	Thr	Leu 320	Ala	Ser	Pro	Glu	Glu 325	Thr	Arg	Cys	His	Phe 330
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Asp	Phe	Gly	Cys	Pro 350	Ala	Thr	Thr	Thr	Thr 355	Ala	Thr	Val	Pro	Thr 360
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35 40 45  
Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu 60  
50 55 60  
Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg 75  
65 70 75  
Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys 90  
80 85 90

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Tyr	Leu	Asp	Leu	Ser 125	Phe	Asn	Asp	Phe	Asp 130	Thr	Met	Pro	Ile	Cys 135
Glu	Glu	Ala	Gly	Asn 140	Met	Ser	His	Leu	Glu 145	Ile	Leu	Gly	Leu	Ser 150
Gly	Ala	Lys	Ile	Gln 155	Lys	Ser	Asp	Phe	Gln 160	Lys	Ile	Ala	His	Leu 165
His	Leu	Asn	Thr	Val 170	Phe	Leu	Gly	Phe	Arg 175	Thr	Leu	Pro	His	Tyr 180
Glu	Glu	Gly	Ser	Leu 185	Pro	Ile	Leu	Asn	Thr 190	Thr	Lys	Leu	His	Ile 195
Val	Leu	Pro	Met	Asp 200	Thr	Asn	Phe	Trp	Val 205	Leu	Leu	Arg	Asp	Gly 210
Ile	Lys	Thr	Ser	Lys 215	Ile	Leu	Glu	Met	Thr 220	Asn	Ile	Asp	Gly	Lys 225
Ser	Gln	Phe	Val	Ser 230	Tyr	Glu	Met	Gln	Arg 235	Asn	Leu	Ser	Leu	Glu 240
Asn	Ala	Lys	Thr	Ser 245	Val	Leu	Leu	Leu	Asn 250	Lys	Val	Asp	Leu	Leu 255
Trp	Asp	Asp	Leu	Phe 260	Leu	Ile	Leu	Gln	Phe 265	Val	Trp	His	Thr	Ser 270
Val	Glu	His	Phe	Gln 275	Ile	Arg	Asn	Val	Thr 280	Phe	Gly	Gly	Lys	Ala 285
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Thr	Ile	Lys	Leu	Glu 305	His	Val	His	Phe	Arg 310	Val	Phe	Tyr	Ile	Gln 315
Gln	Asp	Lys	Ile	Tyr 320	Leu	Leu	Leu	Thr	Lys 325	Met	Asp	Ile	Glu	Asn 330
Leu	Thr	Ile	Ser	Asn 335	Ala	Gln	Met	Pro	His 340	Met	Leu	Phe	Pro	Asn 345
Tyr	Pro	Thr	Lys	Phe 350	Gln	Tyr	Leu	Asn	Phe 355	Ala	Asn	Asn	Ile	Leu 360
Thr	Asp	Glu	Leu	Phe 365	Lys	Arg	Thr	Ile	Gln 370	Leu	Pro	His	Leu	Lys 375
Thr	Leu	Ile	Leu	Asn 380	Gly	Asn	Lys	Leu	Glu 385	Thr	Leu	Ser	Leu	Val 390
Ser	Cys	Phe	Ala	Asn 395	Asn	Thr	Pro	Leu	Glu 400	His	Leu	Asp	Leu	Ser 405

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Glu	Thr	Val	Val	Asn	Met	Asn	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Asp	
				425					430					435	
Ser	Val	Phe	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Gln	Ile	Leu	Asp	Leu	
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Asn	Asn	Asn	Gln	Ile	Gln	Thr	Val	Pro	Lys	Glu	Thr	Ile	His	Leu	
				455					460					465	
Met	Ala	Leu	Arg	Glu	Leu	Asn	Ile	Ala	Phe	Asn	Phe	Leu	Thr	Asp	
				470					475					480	
Leu	Pro	Gly	Cys	Ser	His	Phe	Ser	Arg	Leu	Ser	Val	Leu	Asn	Ile	
				485					490					495	
Glu	Met	Asn	Phe	Ile	Leu	Ser	Pro	Ser	Leu	Asp	Phe	Val	Gln	Ser	
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Cys	Gln	Glu	Val	Lys	Thr	Leu	Asn	Ala	Gly	Arg	Asn	Pro	Phe	Arg	
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Cys	Thr	Cys	Glu	Leu	Lys	Asn	Phe	Ile	Gln	Leu	Glu	Thr	Tyr	Ser	
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Glu	Val	Met	Met	Val	Gly	Trp	Ser	Asp	Ser	Tyr	Thr	Cys	Glu	Tyr	
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Pro	Leu	Asn	Leu	Arg	Gly	Thr	Arg	Leu	Lys	Asp	Val	His	Leu	His	
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Glu	Leu	Ser	Cys	Asn	Thr	Ala	Leu	Leu	Ile	Val	Thr	Ile	Val	Val	
				575					580					585	
Ile	Met	Leu	Val	Leu	Gly	Leu	Ala	Val	Ala	Phe	Cys	Cys	Leu	His	
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Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu	Gly	Gln	Cys	Thr	Gln	
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Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser	
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Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu	Glu	Lys	Glu	Asp	
				650					655					660	
Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro	Gly	
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Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr	
				680					685					690	
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp	
				695					700					705	
Cys	His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	
				710					715					720	



Asn	Ser	Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe
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Tyr	Cys	Ile	Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu
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Lys	Lys	Ala	Tyr	Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly
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Leu	Phe	Trp	Ala	Asn	Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu
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Ala	Thr	Arg	Glu	Met	Tyr	Glu	Leu	Gln	Thr	Phe	Thr	Glu	Leu	Asn
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<210> 59  
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<210> 61  
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 <213> Homo sapiens

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 Tyr Tyr Ala Arg Pro Glu Pro Glu Leu Glu Thr Phe Ser Pro Pro  
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 Arg Glu Lys Ser Ala Pro Glu Pro Pro Pro Pro Gly Lys His Ser  
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 Asn Lys Lys Val Met Arg Thr Lys Ser Ser Glu Lys Ala Ala Asn  
                     110                    115                    120  
 Asp Asp His Ser Val Arg Val Ala Arg Glu Asp Val Arg Glu Ser  
                     125                    130                    135  
 Cys Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln  
                     140                    145                    150  
 Leu His Ala Ser Thr Val Lys Arg Tyr Gly Leu Gly Ala His Arg  
                     155                    160                    165  
 Gly Arg Leu Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr  
                     170                    175                    180  
 Asp Gly Ala Trp Cys Ala Gly Arg Asn Asp Leu Gln Gln Trp Ile

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Glu	Val	Asp	Ala	Arg 200	Arg	Leu	Thr	Arg	Phe 205	Thr	Gly	Val	Ile	Thr 210
Gln	Gly	Arg	Asn	Ser 215	Leu	Trp	Leu	Ser	Asp 220	Trp	Val	Thr	Ser	Tyr 225
Lys	Val	Met	Val	Ser 230	Asn	Asp	Ser	His	Thr 235	Trp	Val	Thr	Val	Lys 240
Asn	Gly	Ser	Gly	Asp 245	Met	Ile	Phe	Glu	Gly 250	Asn	Ser	Glu	Lys	Glu 255
Ile	Pro	Val	Leu	Asn 260	Glu	Leu	Pro	Val	Pro 265	Met	Val	Ala	Arg	Tyr 270
Ile	Arg	Ile	Asn	Pro 275	Gln	Ser	Trp	Phe	Asp 280	Asn	Gly	Ser	Ile	Cys 285
Met	Arg	Met	Glu	Ile 290	Leu	Gly	Cys	Pro	Leu 295	Pro	Asp	Pro	Asn	Asn 300
Tyr	Tyr	His	Arg	Arg 305	Asn	Glu	Met	Thr	Thr 310	Thr	Asp	Asp	Leu	Asp 315
Phe	Lys	His	His	Asn 320	Tyr	Lys	Glu	Met	Arg 325	Gln	Leu	Met	Lys	Val 330
Val	Asn	Glu	Met	Cys 335	Pro	Asn	Ile	Thr	Arg 340	Ile	Tyr	Asn	Ile	Gly 345
Lys	Ser	His	Gln	Gly 350	Leu	Lys	Leu	Tyr	Ala 355	Val	Glu	Ile	Ser	Asp 360
His	Pro	Gly	Glu	His 365	Glu	Val	Gly	Glu	Pro 370	Glu	Phe	His	Tyr	Ile 375
Ala	Gly	Ala	His	Gly 380	Asn	Glu	Val	Leu	Gly 385	Arg	Glu	Leu	Leu	Leu 390
Leu	Leu	Val	Gln	Phe 395	Val	Cys	Gln	Glu	Tyr 400	Leu	Ala	Arg	Asn	Ala 405
Arg	Ile	Val	His	Leu 410	Val	Glu	Glu	Thr	Arg 415	Ile	His	Val	Leu	Pro 420
Ser	Leu	Asn	Pro	Asp 425	Gly	Tyr	Glu	Lys	Ala 430	Tyr	Glu	Gly	Gly	Ser 435
Glu	Leu	Gly	Gly	Trp 440	Ser	Leu	Gly	Arg	Trp 445	Thr	His	Asp	Gly	Ile 450
Asp	Ile	Asn	Asn	Asn 455	Phe	Pro	Asp	Leu	Asn 460	Thr	Leu	Leu	Trp	Glu 465
Ala	Glu	Asp	Arg	Gln 470	Asn	Val	Pro	Arg	Lys 475	Val	Pro	Asn	His	Tyr 480
Ile	Ala	Ile	Pro	Glu 485	Trp	Phe	Leu	Ser	Glu 490	Asn	Ala	Thr	Val	Ala 495
Ala	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp	Met	Glu	Lys	Ile	Pro	Phe

500										505					510				
Val	Leu	Gly	Gly	Asn	Leu	Gln	Gly	Gly	Glu	Leu	Val	Val	Ala	Tyr					
				515					520					525					
Pro	Tyr	Asp	Leu	Val	Arg	Ser	Pro	Trp	Lys	Thr	Gln	Glu	His	Thr					
				530					535					540					
Pro	Thr	Pro	Asp	Asp	His	Val	Phe	Arg	Trp	Leu	Ala	Tyr	Ser	Tyr					
				545					550					555					
Ala	Ser	Thr	His	Arg	Leu	Met	Thr	Asp	Ala	Arg	Arg	Arg	Val	Cys					
				560					565					570					
His	Thr	Glu	Asp	Phe	Gln	Lys	Glu	Glu	Gly	Thr	Val	Asn	Gly	Ala					
				575					580					585					
Ser	Trp	His	Thr	Val	Ala	Gly	Ser	Leu	Asn	Asp	Phe	Ser	Tyr	Leu					
				590					595					600					
His	Thr	Asn	Cys	Phe	Glu	Leu	Ser	Ile	Tyr	Val	Gly	Cys	Asp	Lys					
				605					610					615					
Tyr	Pro	His	Glu	Ser	Gln	Leu	Pro	Glu	Glu	Trp	Glu	Asn	Asn	Arg					
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Glu	Ser	Leu	Ile	Val	Phe	Met	Glu	Gln	Val	His	Arg	Gly	Ile	Lys					
				635					640					645					
Gly	Leu	Val	Arg	Asp	Ser	His	Gly	Lys	Gly	Ile	Pro	Asn	Ala	Ile					
				650					655					660					
Ile	Ser	Val	Glu	Gly	Ile	Asn	His	Asp	Ile	Arg	Thr	Ala	Asn	Asp					
				665					670					675					
Gly	Asp	Tyr	Trp	Arg	Leu	Leu	Asn	Pro	Gly	Glu	Tyr	Val	Val	Thr					
				680					685					690					
Ala	Lys	Ala	Glu	Gly	Phe	Thr	Ala	Ser	Thr	Lys	Asn	Cys	Met	Val					
				695					700					705					
Gly	Tyr	Asp	Met	Gly	Ala	Thr	Arg	Cys	Asp	Phe	Thr	Leu	Ser	Lys					
				710					715					720					
Thr	Asn	Met	Ala	Arg	Ile	Arg	Glu	Ile	Met	Glu	Lys	Phe	Gly	Lys					
				725					730					735					
Gln	Pro	Val	Ser	Leu	Pro	Ala	Arg	Arg	Leu	Lys	Leu	Arg	Gly	Arg					
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Lys	Arg	Arg	Gln	Arg	Gly														
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<220>  
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<210> 64  
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<220>  
<223> Synthetic oligonucleotide probe

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<210> 65  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 66  
<211> 2854  
<212> DNA  
<213> Homo sapiens

<400> 66  
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cccagccccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150  
cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200  
gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250  
cgtgggacct gccagtgtc tgtttccctg ccagacacca cctttcccgt 300  
ggacagagtg gaacgcttgg aattcacagc tcatgttctt tctcagaagt 350  
ttgagaaaga actttctaaa gtgaggaat atgtccaatt aattagtgtg 400  
tatgaaaaga aactgttaaa cctaactgtc cgaattgaca tcatggagaa 450  
ggataccatt tcttacctg aactggactt cgagctgac aaggtagaag 500  
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aaagatcaaa acaccctgt cgtccaccct cctcccactc caggagctg 750  
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 ggtacagcag tttaacaaca caacatgtac gtcaacatgt acaacaccgg 1050  
 gaatattgcc agagttaacc tgaccaccaa cacgattgct gtgactcaaa 1100  
 ctctccctaa tgctgcctat aataaccgct tttcatatgc taatgttgct 1150  
 tggcaagata ttgactttgc tgtggatgag aatggattgt ggggttattta 1200  
 ttcaactgaa gccagcactg gtaacatggt gattagtaaa ctcaatgaca 1250  
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 gcttctaacg ccttcatggt atgtgggggt ctgtatgcca ccctactat 1350  
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Ala	Ile	Arg	Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu	215	220	225
Cys	Glu	Ala	Ser	Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro	230	235	240
Pro	Thr	Pro	Gly	Ser	Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser	245	250	255
Lys	Pro	Ser	Val	Val	Gln	Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu	260	265	270
Tyr	Gly	Ala	Trp	Gly	Arg	Asp	Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys	275	280	285
Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu	Asn	Thr	Asp	Gly	Arg	Leu	Leu	290	295	300
Glu	Tyr	Tyr	Arg	Leu	Tyr	Asn	Thr	Leu	Asp	Asp	Leu	Leu	Leu	Tyr	305	310	315
Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr	Gly	Gln	Gly	Ser	Gly	320	325	330
Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr	335	340	345
Gly	Asn	Ile	Ala	Arg	Val	Asn	Leu	Thr	Thr	Asn	Thr	Ile	Ala	Val	350	355	360
Thr	Gln	Thr	Leu	Pro	Asn	Ala	Ala	Tyr	Asn	Asn	Arg	Phe	Ser	Tyr	365	370	375
Ala	Asn	Val	Ala	Trp	Gln	Asp	Ile	Asp	Phe	Ala	Val	Asp	Glu	Asn	380	385	390
Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Ala	Ser	Thr	Gly	Asn	Met	395	400	405
Val	Ile	Ser	Lys	Leu	Asn	Asp	Thr	Thr	Leu	Gln	Val	Leu	Asn	Thr	410	415	420
Trp	Tyr	Thr	Lys	Gln	Tyr	Lys	Pro	Ser	Ala	Ser	Asn	Ala	Phe	Met	425	430	435
Val	Cys	Gly	Val	Leu	Tyr	Ala	Thr	Arg	Thr	Met	Asn	Thr	Arg	Thr	440	445	450
Glu	Glu	Ile	Phe	Tyr	Tyr	Tyr	Asp	Thr	Asn	Thr	Gly	Lys	Glu	Gly	455	460	465
Lys	Leu	Asp	Ile	Val	Met	His	Lys	Met	Gln	Glu	Lys	Val	Gln	Ser	470	475	480
Ile	Asn	Tyr	Asn	Pro	Phe	Asp	Gln	Lys	Leu	Tyr	Val	Tyr	Asn	Asp	485	490	495
Gly	Tyr	Leu	Leu	Asn	Tyr	Asp	Leu	Ser	Val	Leu	Gln	Lys	Pro	Gln	500	505	510

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 <211> 410  
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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ggtgaacatc agcaaaccgt ctgtggttca gctcaactgg agagggtttt 150

cttatctata tgggtgcttg ggtagggatt actctcccca gcatccaaac 200

aaaggnatgt attggngngc gccattgaat acagatggga gactgttgga 250

gtattataga ctgtacaacc cactggatga tttgctattg tatataaatg 300

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taacctgacc 410

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

agctgtggtc atggtggtgt ggtg 24

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctaccttggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

catcagcaaa ccgtctgtgg ttcagotcaa ctggagaggg tt 42

<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

<400> 72

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tggggctgtg ctccatggcg agctggatac catgtttgtg tggaagtgcc 150  
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tagattgatc tatgcacttt tcttgcttgt tggagtatgt gtagcttgtg 250  
taatgttgat accaggaatg gaagaacaac tgaataagat tcctggattt 300  
tgtgagaatg agaaagggtg tgtcccttgt aacattttgg ttggctataa 350  
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 cggtagctaaa ttgaataacg agtaaataat cttacttggg tagagatggc 2050  
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 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 73

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Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Leu	Leu	Cys	Arg	Cys	Cys	Pro	
				20					25					30	
Ser	Gly	Asn	Asn	Ser	Thr	Val	Thr	Arg	Leu	Ile	Tyr	Ala	Leu	Phe	
				35					40					45	
Leu	Leu	Val	Gly	Val	Cys	Val	Ala	Cys	Val	Met	Leu	Ile	Pro	Gly	
				50					55					60	
Met	Glu	Glu	Gln	Leu	Asn	Lys	Ile	Pro	Gly	Phe	Cys	Glu	Asn	Glu	
				65					70					75	
Lys	Gly	Val	Val	Pro	Cys	Asn	Ile	Leu	Val	Gly	Tyr	Lys	Ala	Val	
				80					85					90	
Tyr	Arg	Leu	Cys	Phe	Gly	Leu	Ala	Met	Phe	Tyr	Leu	Leu	Leu	Ser	
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Leu	Leu	Met	Ile	Lys	Val	Lys	Ser	Ser	Ser	Asp	Pro	Arg	Ala	Ala	
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Val	His	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Ala	Ala	Ala	Ile	Ala	
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Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	Gly	Thr	Phe	Thr	Thr	
				140					145					150	
Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	Cys	Phe	Ile	Leu	
				155					160					165	
Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Glu	
				170					175					180	
Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	Trp	Tyr	
				185					190					195	
Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	Leu	
				200					205					210	
Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser	
				215					220					225	
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys	
				230					235					240	
Val	Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser	
				245					250					255	
Gln	Pro	Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr	
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Thr	Met	Tyr	Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr	
				275					280					285	

Asn	Cys	Asn	Pro	Ser	Leu	Leu	Ser	Ile	Ile	Gly	Tyr	Asn	Thr	Thr	290	295	300
Ser	Thr	Val	Pro	Lys	Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala	305	310	315
Gln	Gly	Ile	Ile	Gly	Leu	Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr	320	325	330
Ser	Ser	Ile	Arg	Thr	Ser	Asn	Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr	335	340	345
Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	Ile	Glu	Asp	Gly	Gly	Ala	Arg	350	355	360
Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	Asp	Val	His	Arg	Ala	Val	365	370	375
Asp	Asn	Glu	Arg	Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	380	385	390
Phe	Met	Leu	Phe	Leu	Ala	Ser	Leu	Tyr	Ile	Met	Met	Thr	Leu	Thr	395	400	405
Asn	Trp	Ser	Arg	Tyr	Glu	Pro	Ser	Arg	Glu	Met	Lys	Ser	Gln	Trp	410	415	420
Thr	Ala	Val	Trp	Val	Lys	Ile	Ser	Ser	Ser	Trp	Ile	Gly	Ile	Val	425	430	435
Leu	Tyr	Val	Trp	Thr	Leu	Val	Ala	Pro	Leu	Val	Leu	Thr	Asn	Arg	440	445	450

Asp Phe Asp

<210> 74  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 48, 163  
 <223> unknown base

<400> 74  
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 ataccatggt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150  
 tagtggaac aantccactg taactagatt gatctatgca cttttcttgc 200  
 ttgttgagat atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250  
 caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300  
 ttgtaacatt ttggttggt ataaagctgt atatcgtttg tgctttggtt 350  
 tggctatggt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400





<210> 77  
<211> 666  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 21, 111  
<223> unknown base

<400> 77  
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caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150  
gaaagggtgtt gtcccccttg aacatttttg gttggctata aagctgtata 200  
tcgtttgtgc tttgggttggt ctatgttcta tcttcttctc tctttactaa 250  
tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300  
ttttgggttct ttaaatttgc tgcagcaatt gcaattatta ttggggcatt 350  
cttcattcca gaaggaactt ttacaactgt gtggttttat gtaggcatgg 400  
cagggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450  
gcacattcat ggaatgaatc gtggggttgaa aaaatggaag aagggaactc 500  
gagatgttgg tatgcagcct tgttatcagc tacagctctg aattatctgc 550  
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tggtgcttct gtaatg 666

<210> 78  
<211> 22  
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<220>  
<223> Synthetic oligonucleotide probe

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<210> 79  
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<212> DNA  
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<220>  
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<400> 79  
gtcaacatgc tcctctgc 18

<210> 80  
<211> 26

<212> DNA  
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<220>  
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aatccattgt gcaactgcagc tctagg 26

<210> 81  
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<223> Synthetic oligonucleotide probe

<400> 81  
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<210> 82  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
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gcac 54

<210> 83  
<211> 3906  
<212> DNA  
<213> Homo sapiens

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gcacacaagg ctctggctcg cttccctccc tcgtttccag ctctggggcg 450  
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 ttctgtagca caccatgtg ctgcccctca cgtcctcca tcctcactgg 900  
 caagtacgtc cacaaccaca acaccta cac caaatgag aactgctcct 950  
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 gaaaaa 3906

<210> 84  
 <211> 867  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 20 25 30  
 Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn  
 35 40 45  
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser  
 50 55 60  
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly  
 65 70 75  
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro  
 80 85 90  
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn  
 95 100 105  
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala  
 110 115 120  
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly  
 125 130 135  
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly  
 140 145 150  
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys  
 155 160 165  
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys  
 170 175 180  
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu  
 185 190 195  
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met  
 200 205 210  
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro  
 215 220 225  
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro  
 230 235 240  
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn  
 245 250 255



Pro	Glu	Asp	Gln	Asp	Asp	Lys	Asp	Gly	Gly	Asp	Phe	Ser	Gly	Thr	575	580	585
Gly	Gly	Leu	Pro	Asp	Tyr	Ser	Ala	Ala	Asn	Pro	Ile	Lys	Val	Thr	590	595	600
His	Arg	Cys	Tyr	Ile	Leu	Glu	Asn	Asp	Thr	Val	Gln	Cys	Asp	Leu	605	610	615
Asp	Leu	Tyr	Lys	Ser	Leu	Gln	Ala	Trp	Lys	Asp	His	Lys	Leu	His	620	625	630
Ile	Asp	His	Glu	Ile	Glu	Thr	Leu	Gln	Asn	Lys	Ile	Lys	Asn	Leu	635	640	645
Arg	Glu	Val	Arg	Gly	His	Leu	Lys	Lys	Lys	Arg	Pro	Glu	Glu	Cys	650	655	660
Asp	Cys	His	Lys	Ile	Ser	Tyr	His	Thr	Gln	His	Lys	Gly	Arg	Leu	665	670	675
Lys	His	Arg	Gly	Ser	Ser	Leu	His	Pro	Phe	Arg	Lys	Gly	Leu	Gln	680	685	690
Glu	Lys	Asp	Lys	Val	Trp	Leu	Leu	Arg	Glu	Gln	Lys	Arg	Lys	Lys	695	700	705
Lys	Leu	Arg	Lys	Leu	Leu	Lys	Arg	Leu	Gln	Asn	Asn	Asp	Thr	Cys	710	715	720
Ser	Met	Pro	Gly	Leu	Thr	Cys	Phe	Thr	His	Asp	Asn	Gln	His	Trp	725	730	735
Gln	Thr	Ala	Pro	Phe	Trp	Thr	Leu	Gly	Pro	Phe	Cys	Ala	Cys	Thr	740	745	750
Ser	Ala	Asn	Asn	Asn	Thr	Tyr	Trp	Cys	Met	Arg	Thr	Ile	Asn	Glu	755	760	765
Thr	His	Asn	Phe	Leu	Phe	Cys	Glu	Phe	Ala	Thr	Gly	Phe	Leu	Glu	770	775	780
Tyr	Phe	Asp	Leu	Asn	Thr	Asp	Pro	Tyr	Gln	Leu	Met	Asn	Ala	Val	785	790	795
Asn	Thr	Leu	Asp	Arg	Asp	Val	Leu	Asn	Gln	Leu	His	Val	Gln	Leu	800	805	810
Met	Glu	Leu	Arg	Ser	Cys	Lys	Gly	Tyr	Lys	Gln	Cys	Asn	Pro	Arg	815	820	825
Thr	Arg	Asn	Met	Asp	Leu	Asp	Gly	Gly	Ser	Tyr	Glu	Gln	Tyr	Arg	830	835	840
Gln	Phe	Gln	Arg	Arg	Lys	Trp	Pro	Glu	Met	Lys	Arg	Pro	Ser	Ser	845	850	855
Lys	Ser	Leu	Gly	Gln	Leu	Trp	Glu	Gly	Trp	Glu	Gly				860	865	

<210> 85  
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 <212> DNA

<213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 85  
 gaagccggct gtctgaatc 19  
 <210> 86  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic oligonucleotide probe  
 <400> 86  
 ggccagctat ctccgcag 18  
 <210> 87  
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 <212> DNA  
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 <400> 87  
 aagggcctgc aagagaag 18  
 <210> 88  
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<210> 91  
<211> 24  
<212> DNA  
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<400> 91  
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<210> 92  
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<220>  
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<400> 92  
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<210> 93  
<211> 45  
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<210> 94  
<211> 971  
<212> DNA  
<213> Homo sapiens

<400> 94  
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 ccctgagaat gtccttttgg tttggagaag gcagtgtgag gctgcacagt 900  
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 aaaaaaaaaa aaaaaaaaaa a 971

<210> 95  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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                     20                    25                    30  
 Cys Leu Phe His Gly Arg Gln Asp Cys Asp Val Glu Arg Asn Arg  
                     35                    40                    45  
 Thr Ala Ala Gly Gly Asn Arg Val Arg Arg Ala Gln Pro Trp Pro  
                     50                    55                    60  
 Phe Arg Arg Arg Gly His Leu Gly Ile Phe His His His Arg His  
                     65                    70                    75  
 Pro Gly His Val Ser His Val Pro Asn Val Gly Leu His His His  
                     80                    85                    90  
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 Pro His Arg His His Pro Arg His Ala Arg  
                     110                    115

<210> 96  
 <211> 1312  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
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aaaaaaaaaa	aa	1312			

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<210> 97
<211> 313
<212> PRT
<213> Homo sapiens
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<400> 97
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Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
          35          40
Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr
          50          55
Gly Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg
          65          70          75

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Ser	Ile	Ala	Val	Tyr	Tyr	Asp	Asn	Pro	His	Met	Val	Pro	Pro	Asp	80	85	90
Lys	Cys	Arg	Cys	Ala	Val	Gly	Ser	Ile	Leu	Ser	Glu	Gly	Glu	Glu	95	100	105
Ser	Pro	Ser	Pro	Glu	Leu	Ile	Asp	Leu	Tyr	Gln	Lys	Phe	Gly	Phe	110	115	120
Lys	Val	Phe	Ser	Phe	Pro	Ala	Pro	Ser	His	Val	Val	Thr	Ala	Thr	125	130	135
Phe	Pro	Tyr	Thr	Thr	Ile	Leu	Ser	Ile	Trp	Leu	Ala	Thr	Arg	Arg	140	145	150
Val	His	Pro	Ala	Leu	Asp	Thr	Tyr	Ile	Lys	Glu	Arg	Lys	Leu	Cys	155	160	165
Ala	Tyr	Pro	Arg	Leu	Glu	Ile	Tyr	Gln	Glu	Asp	Gln	Ile	His	Phe	170	175	180
Met	Cys	Pro	Leu	Ala	Arg	Gln	Gly	Asp	Phe	Tyr	Val	Pro	Glu	Met	185	190	195
Lys	Glu	Thr	Glu	Trp	Lys	Trp	Arg	Gly	Leu	Val	Glu	Ala	Ile	Asp	200	205	210
Thr	Gln	Val	Asp	Gly	Thr	Gly	Ala	Asp	Thr	Met	Ser	Asp	Thr	Ser	215	220	225
Ser	Val	Ser	Leu	Glu	Val	Ser	Pro	Gly	Ser	Arg	Glu	Thr	Ser	Ala	230	235	240
Ala	Thr	Leu	Ser	Pro	Gly	Ala	Ser	Ser	Arg	Gly	Trp	Asp	Asp	Gly	245	250	255
Asp	Thr	Arg	Ser	Glu	His	Ser	Tyr	Ser	Glu	Ser	Gly	Ala	Ser	Gly	260	265	270
Ser	Ser	Phe	Glu	Glu	Leu	Asp	Leu	Glu	Gly	Glu	Gly	Pro	Leu	Gly	275	280	285
Glu	Ser	Arg	Leu	Asp	Pro	Gly	Thr	Glu	Pro	Leu	Gly	Thr	Thr	Lys	290	295	300
Trp	Leu	Trp	Glu	Pro	Thr	Ala	Pro	Glu	Lys	Gly	Lys	Glu			305	310	

<210> 98  
 <211> 725  
 <212> DNA  
 <213> Homo sapiens

<400> 98  
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 cccgtcccat ctgtgtgtgc tgtgtgtgt cagtgcggcg gtgtgccggg 150  
 ctgaggctgg gctcgaaacc gaaagtcccg tccggaccct ccaagtggag 200  
 accctggtgg agccccaga accatgtgcc gagcccgtg cttttggaga 250

cacgcttcac atacactaca cggaagctt ggtagatgga cgtattattg 300  
 acacctccct gaccagagac cctctggta tagaacttgg ccaaaagcag 350  
 gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400  
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 gcaactatcc gagccaacta ctggctaaag ctggtgaagg gcattttgcc 550  
 tctggtaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600  
 acctatacag aaaggccaat agacccaaag tctccaaaaa gaagctcaag 650  
 gaagagaaac gaaacaagag caaaaagaaa taataaataa taaattttta 700  
 aaaacttaaa aaaaaaaaaa aaaaa 725

<210> 99  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 99  
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 20 25  
 Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu 45  
 35 40  
 Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu 60  
 50 55  
 His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp 75  
 65 70  
 Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys 90  
 80 85  
 Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val 105  
 95 100  
 Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly 120  
 110 115  
 Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln 135  
 125 130  
 Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu 150  
 140 145  
 Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly Met Ala Met Val 165  
 155 160  
 Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala 180  
 170 175  
 Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu Glu Lys Arg

Asn Lys Ser Lys Lys Lys  
200

<210> 100  
<211> 705  
<212> DNA  
<213> Homo sapiens

<400> 100  
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cgctccatct gctgctgctg ctgctgctca gtgcggcggg gtgccgggct 150  
gaggctgggc tcgaaaccga aagtcccgtc cggaccctcc aagtggagac 200  
cctggtggag cccccagaac catgtgccga gcccgctgct tttggagaca 250  
cgcttcacat aactacacg ggaagcttgg tagatggacg tattattgac 300  
acctccctga ccagagaccc tctggttata gaacttggcc aaaagcaggt 350  
gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400  
gaagggaat cattccttct cacttggcct atggaaaacg gggatttcca 450  
ccatctgtcc cagcggatgc agtgggtgcag tatgacgtgg agctgattgc 500  
actaatccga gccaaactact ggctaaagct ggtgaagggc attttgcctc 550  
tggtagggat ggccatggtg ccaccctcct gggcctcatt gggatcacc 600  
tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650  
gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700  
actta 705

<210> 101  
<211> 543  
<212> DNA  
<213> Homo sapiens

<400> 101  
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gaaccatgtg ccgagcccgcc tgcttttggg gacacgcttc acatacacta 100  
cacgggaagc ttggtagatg gacgtattat tgacacctcc ctgaccagag 150  
accctctggt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200  
cagagtcttc tcgacatgtg tgtgggagag aagcgaaggc caatcattcc 250  
ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300  
atgcagtggg gcagtatgac gtggagctga ttgcactaat ccgagccaac 350  
tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

ggtgccagcc ctcttgggcc tcattgggta tcacctatac agaaaggcca 450  
 atagacccaa agtctccaaa aagaagctca aggaagagaa acgaaacaag 500  
 agcaaaaaga aataataaat aataaatttt aaaaaactta aaa 543

<210> 102  
 <211> 1316  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
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 aaatcggggg agtgaggcgg gccggcgcg cgcgacaccg ggctccggaa 100  
 ccaactgcacg acggggctgg actgacctga aaaaaatgtc tggatttcta 150  
 gagggcttga gatgctcaga atgcattgac tggggggaaa agcgcaatac 200  
 tattgcttcc attgctgctg gtgtactatt ttttacaggc tgggtggatta 250  
 tcatagatgc agctgttatt tatccacca tgaaagattt caaccactca 300  
 taccatgcct gtggtgttat agcaaccata gccttcctaa tgattaatgc 350  
 agtatcgaat ggacaagtcc gaggtgatag ttacagtga gggtgtctgg 400  
 gtcaaacagg tgctgcatt tggcttttcg ttggtttcat gttggccttt 450  
 ggatctctga ttgcatctat gtggattcct tttggagggt atgttgctaa 500  
 agaaaaagac atagtatacc ctggaattgc tgtatttttc cagaatgcct 550  
 tcatcttttt tggagggtcg gtttttaagt ttggccgcac tgaagactta 600  
 tggcagtga cacatctgat ttcccacagc acaacagccc tgcattgggt 650  
 tgtttgtttt tttactgctc actcccaacc ttttgtaatg ccattttcta 700  
 aacttatttc tgagtgtagt ctgagcttaa agttgtgtaa tactaaaatc 750  
 acgagaacac ctaaacaaca accaaaaatc tattgtggta tgcacttgat 800  
 taacttataa aatgttagag gaaactttca catgaataat ttttgcataa 850  
 ttttatcatg gtataatttg taaaaataaa aagaaattac aaaagaaatt 900  
 atggatttgt caatgtaagt atttgcata tctgagggtc aaaaccacaa 950  
 tgaaagtgc ctgaagattt aatgtgttta ttcaaattgt gtctcttctg 1000  
 tgtcaaattg taaatgaaat ataaacattt tttagttttt aaaatattcc 1050  
 gtggtcaaaa ttcttctca ctataattgg tatttacttt taccaaaaat 1100  
 tctgtgaaca tgtaatgtaa ctggcttttg aggggtctccc aaggggtgag 1150  
 tggacgtgtt ggaagagaga agcaccatgg tccagccacc aggtccctg 1200  
 tgtcccttcc atgggaaggt cttccgctgt gcctctcatt ccaagggcag 1250  
 gaagatgtga ctgagccatg acacgtgggt ctggtgggat gcacagtcac 1300

tccacatcca ccactg 1316

<210> 103  
<211> 157  
<212> PRT  
<213> Homo sapiens

<400> 103  
Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp  
1 5 10 15  
Trp Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val  
20 25 30  
Leu Phe Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile  
35 40 45  
Tyr Pro Thr Met Lys Asp Phe Asn His Ser Tyr His Ala Cys Gly  
50 55 60  
Val Ile Ala Thr Ile Ala Phe Leu Met Ile Asn Ala Val Ser Asn  
65 70 75  
Gly Gln Val Arg Gly Asp Ser Tyr Ser Glu Gly Cys Leu Gly Gln  
80 85 90  
Thr Gly Ala Arg Ile Trp Leu Phe Val Gly Phe Met Leu Ala Phe  
95 100 105  
Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Gly Tyr Val  
110 115 120  
Ala Lys Glu Lys Asp Ile Val Tyr Pro Gly Ile Ala Val Phe Phe  
125 130 135  
Gln Asn Ala Phe Ile Phe Phe Gly Gly Leu Val Phe Lys Phe Gly  
140 145 150  
Arg Thr Glu Asp Leu Trp Gln  
155

<210> 104  
<211> 545  
<212> DNA  
<213> Homo sapiens

<400> 104  
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tggatttcta gagggcttga gatgctcaga atgcattgac tggggggaaa 150  
agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200  
tggtggatta tcatagatgc agctgttatt tatccaccca tgaaagattt 250  
caaccactca taccatgcct gtggtgttat agcaaccata gccttctaa 300  
tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagtga 350  
ggttgtctgg gtcaaacagg tgctcgcat tggcttttcg ttggtttcat 400



gttggccttt ggatctctga ttgcatctat gtggattctt tttggagggt 450  
 atgttgctaa agaaaaagac atagtatacc ctggaattgc tgtatttttc 500  
 cagaatgcct tcatcttttt tggagggctg gtttttaagt ttggc 545

<210> 105  
 <211> 490  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 31, 39, 108, 145, 179, 219, 412, 479  
 <223> unknown base

<400> 105  
 tggacggacc tgaaaaaat gtttggattt ntagaggnt tgagatgttc 50  
 agaatgcatg actgggggaa aagcgcaaat actattgctt ccattgctgc 100  
 tgggtganta ttttttacag gctggtggat tatcatagat gcagntgtta 150  
 tttatccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200  
 atagcaacca tagccttont aatgattaat gcagtatcga atggacaagt 250  
 ccgaggtgat agttacagtg aaggttgttt gggtaaaca ggtgctcgca 300  
 tttggctttt cgttggtttc atgttggcct ttggatctct gattgcatct 350  
 atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 400  
 ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450  
 tggtttttaa gtttggccgc actgaagant tatggcagtg 490

<210> 106  
 <211> 466  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 26, 38, 81, 115, 207, 329, 380, 446, 449  
 <223> unknown base

<400> 106  
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 aatgtttgga ttttttagagg gcttgagatg ntcagaatgc attgactggg 100  
 ggaaaagcgc aatantattg ctttccattg ctgctggtgt actatttttt 150  
 acaggggtggg ggattatcat agatgcagct gttatttatc ccacatgaa 200  
 agatttnaac cactcatacc atgcctgtgg tgttatagca accatagcct 250  
 tcctaataatg taatgcagta tcgaatggac aagtccgagg tgatagttac 300  
 agtgaagggtt gtttgggtca aacaggtgnt cgcatttggc ttttcgttgg 350  
 tttcatgttg gcctttggat ttctgattgn attctatgcg gattcttctt 400

ggagggttatg ttgctaaaga aaaagacata gtataccctg gaattnctnt 450  
atttttccag aatgcc 466

<210> 107

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356

<223> unknown base

<400> 107

tagagggctt gagatgctca gaatgcattg actgggggga aaagcgcaat 50

antattgctt ccattgntgn tgggtgnta tttttttaca ggctggtgga 100

ttatnataga tgcagctggtt atttatccca ccatgaaaga ttnaaccan 150

tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcagtatng aatggacaag tccgaggtga tagttacagt gaaggttgtt 250

tgggtcaaac aggtgntngc atttggcttt tngttggttt catgttggcc 300

tttgatctn tgattgcatt tatgtggatt ntttttggag gttatgttgc 350

taaagnaaaa gacatagtat accctgt 377

<210> 108

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 12, 25, 65, 130, 437, 537

<223> unknown base

<400> 108

gggaggctgt gnccgttttg ttttnttggc taaaatcggg ggagtgaggc 50

ggcccggcgc ggcgngacac cgggttccgg gaaccattgc acgacggggt 100

ggactgacct gaaaaaaatg tttggatttn tagagggctt gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200

tgggtgtacta ttttttacag gctggtggat tatcatagat gcagctgtta 250

tttatcccac catgaaagat ttcaaccact cataccatgc ctgtggtgtt 300

atagcaacca tagccttcct aatgattaat gcagtatoga atggacaagt 350

ccgaggtgat agttacagtg aaggttgtct ggggtcaaaca ggtgctcgca 400

tttggctttt cgttggtttc atgttggcct ttggatntct gattgcatct 450

atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 500

ccctggaatt gctgtatttt tccagaatgc cttcatnttt tttggagggc 550

tg 552

<210> 109  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 109  
gggtggatgg tactgctgca tcc 23

<210> 110  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 110  
tgttgtgctg tgggaaatca gatgtg 26

<210> 111  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 111  
gtgtctggag gctgtggccg ttttgttttc ttgggctaaa atcggg 46

<210> 112  
<211> 3004  
<212> DNA  
<213> Homo sapiens

<400> 112  
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ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccttggtaac 150  
tgacaaggag gccaggaaga aggttctcaa acaagctttt tcagccaacc 200  
aagtgccgga gaagctggat gtggtggtaa ttggcagtgg ctttgggggc 250  
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gcagcagctg ggggcctcct ctgagctcca ggagctactc agctacatct 800  
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 aaaa 3004

<210> 113  
 <211> 610  
 <212> PRT  
 <213> Homo sapiens

<400> 113  
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 Val Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro  
 20 25 30  
 Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val  
 35 40 45  
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser  
 50 55 60  
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser  
 65 70 75  
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly  
 80 85 90  
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys  
 95 100 105

Cys	His	Thr	Phe	Gly	Lys	Asn	Gly	Leu	Glu	Phe	Asp	Thr	Gly	Ile	110	115	120
His	Tyr	Ile	Gly	Arg	Met	Glu	Glu	Gly	Ser	Ile	Gly	Arg	Phe	Ile	125	130	135
Leu	Asp	Gln	Ile	Thr	Glu	Gly	Gln	Leu	Asp	Trp	Ala	Pro	Leu	Ser	140	145	150
Ser	Pro	Phe	Asp	Ile	Met	Val	Leu	Glu	Gly	Pro	Asn	Gly	Arg	Lys	155	160	165
Glu	Tyr	Pro	Met	Tyr	Ser	Gly	Glu	Lys	Ala	Tyr	Ile	Gln	Gly	Leu	170	175	180
Lys	Glu	Lys	Phe	Pro	Gln	Glu	Glu	Ala	Ile	Ile	Asp	Lys	Tyr	Ile	185	190	195
Lys	Leu	Val	Lys	Val	Val	Ser	Ser	Gly	Ala	Pro	His	Ala	Ile	Leu	200	205	210
Leu	Lys	Phe	Leu	Pro	Leu	Pro	Val	Val	Gln	Leu	Leu	Asp	Arg	Cys	215	220	225
Gly	Leu	Leu	Thr	Arg	Phe	Ser	Pro	Phe	Leu	Gln	Ala	Ser	Thr	Gln	230	235	240
Ser	Leu	Ala	Glu	Val	Leu	Gln	Gln	Leu	Gly	Ala	Ser	Ser	Glu	Leu	245	250	255
Gln	Ala	Val	Leu	Ser	Tyr	Ile	Phe	Pro	Thr	Tyr	Gly	Val	Thr	Pro	260	265	270
Asn	His	Ser	Ala	Phe	Ser	Met	His	Ala	Leu	Leu	Val	Asn	His	Tyr	275	280	285
Met	Lys	Gly	Gly	Phe	Tyr	Pro	Arg	Gly	Gly	Ser	Ser	Glu	Ile	Ala	290	295	300
Phe	His	Thr	Ile	Pro	Val	Ile	Gln	Arg	Ala	Gly	Gly	Ala	Val	Leu	305	310	315
Thr	Lys	Ala	Thr	Val	Gln	Ser	Val	Leu	Leu	Asp	Ser	Ala	Gly	Lys	320	325	330
Ala	Cys	Gly	Val	Ser	Val	Lys	Lys	Gly	His	Glu	Leu	Val	Asn	Ile	335	340	345
Tyr	Cys	Pro	Ile	Val	Val	Ser	Asn	Ala	Gly	Leu	Phe	Asn	Thr	Tyr	350	355	360
Glu	His	Leu	Leu	Pro	Gly	Asn	Ala	Arg	Cys	Leu	Pro	Gly	Val	Lys	365	370	375
Gln	Gln	Leu	Gly	Thr	Val	Arg	Pro	Gly	Leu	Gly	Met	Thr	Ser	Val	380	385	390
Phe	Ile	Cys	Leu	Arg	Gly	Thr	Lys	Glu	Asp	Leu	His	Leu	Pro	Ser	395	400	405
Thr	Asn	Tyr	Tyr	Val	Tyr	Tyr	Asp	Thr	Asp	Met	Asp	Gln	Ala	Met	410	415	420

Glu Arg Tyr Val	Ser Met Pro Arg Glu	Glu Ala Ala Glu His	Ile
	425	430	435
Pro Leu Leu Phe	Phe Ala Phe Pro Ser	Ala Lys Asp Pro Thr	Trp
	440	445	450
Glu Asp Arg Phe	Pro Gly Arg Ser Thr	Met Ile Met Leu Ile	Pro
	455	460	465
Thr Ala Tyr Glu	Trp Phe Glu Glu Trp	Gln Ala Glu Leu Lys	Gly
	470	475	480
Lys Arg Gly Ser	Asp Tyr Glu Thr Phe	Lys Asn Ser Phe Val	Glu
	485	490	495
Ala Ser Met Ser	Val Val Leu Lys Leu	Phe Pro Gln Leu Glu	Gly
	500	505	510
Lys Val Glu Ser	Val Thr Ala Gly Ser	Pro Leu Thr Asn Gln	Phe
	515	520	525
Tyr Leu Ala Ala	Pro Arg Gly Ala Cys	Tyr Gly Ala Asp His	Asp
	530	535	540
Leu Gly Arg Leu	His Pro Cys Val Met	Ala Ser Leu Arg Ala	Gln
	545	550	555
Ser Pro Ile Pro	Asn Leu Tyr Leu Thr	Gly Gln Asp Ile Phe	Thr
	560	565	570
Cys Gly Leu Val	Gly Ala Leu Gln Gly	Ala Leu Leu Cys Ser	Ser
	575	580	585
Ala Ile Leu Lys	Arg Asn Leu Tyr Ser	Asp Leu Lys Asn Leu	Asp
	590	595	600
Ser Arg Ile Arg	Ala Gln Lys Lys Lys	Asn	
	605	610	

<210> 114  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<400> 114  
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 gatagggctg acgctgctgc tgtgtgcggt gctgctgagc ttggcctcgg 150  
 cgtcctcggg tgaagaaggc agccaggatg aatccttaga ttccaagact 200  
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 agttgctggt caaatatttc ttgattcaga agaattctgaa ttagaatcct 300  
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 acagaagata tcagctttct agagtctcca aatccagaaa acaaggacta 400  
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tacaacctat gactacaaag cagatgaaaa gtgggggcttt tgtgaaactg 600  
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<210> 115

<211> 301

<212> PRT

<213> Homo sapiens

<400> 115

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Leu Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp  
20 25 30





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<210> 117  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<400> 117  
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 Phe Pro Gly Gln Val Ala Gln Leu Ser Cys Thr Leu Ser Pro Gln  
 35 40 45  
 His Val Thr Ile Arg Asp Tyr Gly Val Ser Trp Tyr Gln Gln Arg  
 50 55 60  
 Ala Gly Ser Ala Pro Arg Tyr Leu Leu Tyr Tyr Arg Ser Glu Glu  
 65 70 75  
 Asp His His Arg Pro Ala Asp Ile Pro Asp Arg Phe Ser Ala Ala  
 80 85 90  
 Lys Asp Glu Ala His Asn Ala Cys Val Leu Thr Ile Ser Pro Val  
 95 100 105  
 Gln Pro Glu Asp Asp Ala Asp Tyr Tyr Cys Ser Val Gly Tyr Gly  
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 Phe Ser Pro

<210> 118  
 <211> 3402  
 <212> DNA  
 <213> Homo sapiens

<400> 118

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aa 3402

<210> 119  
<211> 504  
<212> PRT  
<213> Homo sapiens

<400> 119  
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Met Ala Asp Lys Val Val Pro Arg Gln Val Ala Arg Leu Gly Arg  
35 40 45  
Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu  
50 55 60  
Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser  
65 70 75  
Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu  
80 85 90  
Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe  
95 100 105  
Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile  
110 115 120  
Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly  
125 130 135  
Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr  
140 145 150  
Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly  
155 160 165  
Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro  
170 175 180  
Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu  
185 190 195  
Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn  
200 205 210  
Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn  
215 220 225  
Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln  
230 235 240

Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn	245	250	255
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val	260	265	270
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu	275	280	285
Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly	290	295	300
Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro	305	310	315
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln	320	325	330
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly	335	340	345
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys	350	355	360
Pro	Pro	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu	365	370	375
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile	380	385	390
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro	395	400	405
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro	410	415	420
Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu	425	430	435
Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His	440	445	450
Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val	455	460	465
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr	470	475	480
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys	485	490	495
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys							500		

<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

cggttcgaca cgcggcaggt g 21

<210> 122

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

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<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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 <212> PRT  
 <213> Homo sapiens

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 50 55 60  
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 65 70 75  
 Ala Ile Arg Phe Tyr Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu  
 80 85 90  
 Arg Leu Glu Ala Arg Thr Thr Asp Trp Thr Pro Ala Gly Ser Thr  
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 Gly Gln Val Val His Gly Ser Pro Arg Glu Gly Phe Trp Cys Leu  
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 Arg Phe Leu Cys Pro Pro Gly Ser Leu Arg Arg Asp Thr Glu Arg  
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 Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys Cys Ser Ala Ala Cys  
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 Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile Cys Leu Ala Glu  
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 Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly Gln His Cys  
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 Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro Met Gly  
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Gly	Lys	Ser	Ile	Leu 275	Lys	Ile	Thr	Lys	Val 280	Lys	Phe	Ala	Pro	Ile 285
Val	Leu	Thr	Met	Pro 290	Lys	Thr	Ser	Leu	Lys 295	Ala	Ala	Thr	Ile	Lys 300
Ala	Glu	Phe	Val	Arg 305	Ala	Glu	Thr	Pro	Tyr 310	Met	Val	Met	Asn	Pro 315
Glu	Thr	Lys	Ala	Arg 320	Arg	Ala	Gly	Gln	Ser 325	Val	Ser	Leu	Cys	Cys 330
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Cys	Lys	Ala	Gln	Ser 380	Asp	Ala	Gly	Ala	Val 385	Lys	Ser	Lys	Val	Ala 390
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Ala	Thr	Asn	Ser	Phe 425	Tyr	Tyr	Asp	Val	Gly 430	Arg	Cys	Pro	Val	Lys 435
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Phe Val Asp Arg Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu	545	550	555
Pro Phe Asn Lys Lys Gly Ser Ala Val Phe His Glu Ile Lys Met	560	565	570
Leu Arg Arg Lys Glu Pro Ile Thr Leu Glu Ala Met Glu Thr Asn	575	580	585
Ile Ile Pro Leu Gly Glu Val Val Gly Glu Asp Pro Met Ala Glu	590	595	600
Leu Glu Ile Pro Ser Arg Ser Phe Tyr Arg Gln Asn Gly Glu Pro	605	610	615
Tyr Ile Gly Lys Val Lys Ala Ser Val Thr Phe Leu Asp Pro Arg	620	625	630
Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr Asp Leu Asn Phe Ile	635	640	645
Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr Tyr Gly Met Phe	650	655	660
Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro Leu Asn Ala	665	670	675
Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys Met Pro	680	685	690
Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp Thr	695	700	705
Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg	710	715	720
Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu	725	730	735
Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg	740	745	750
Arg Cys Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu	755	760	765
Pro Ser Glu Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu	770	775	780
Glu Pro Arg Thr Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg	785	790	795
Phe Asp Ser Val Ile Thr Gly Pro Asn Gly Ala Cys Val Pro Ala	800	805	810
Phe Cys Asp Asp Gln Ser Pro Asp Ala Tyr Ser Ala Tyr Val Leu	815	820	825
Ala Ser Leu Ala Gly Glu Glu Leu Gln Ala Val Glu Ser Ser Pro	830	835	840



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<211> 438

<212> PRT

<213> Homo sapiens

<400> 129

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Asp	Leu	Cys	Lys	Thr	Gln	Ile	Tyr	Thr	Glu	Glu	Gly	Lys	Val	Trp
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Asp	Tyr	Met	Ala	Cys	Gln	Pro	Glu	Ser	Thr	Asp	Met	Thr	Lys	Tyr
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Leu	Lys	Val	Lys	Leu	Asp	Pro	Pro	Asp	Ile	Thr	Cys	Gly	Asp	Pro
				65					70					75
Pro	Glu	Thr	Phe	Cys	Ala	Met	Gly	Asn	Pro	Tyr	Met	Cys	Asn	Asn
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Glu	Cys	Asp	Ala	Ser	Thr	Pro	Glu	Leu	Ala	His	Pro	Pro	Glu	Leu
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Met	Phe	Asp	Phe	Glu	Gly	Arg	His	Pro	Ser	Thr	Phe	Trp	Gln	Ser
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Ala	Thr	Trp	Lys	Glu	Tyr	Pro	Lys	Pro	Leu	Gln	Val	Asn	Ile	Thr



[illegible]

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Cys	Gln	Cys	Pro	Ala	Ala	Met	Ala	Phe	Cys	Phe	Leu	Glu	Thr	Leu	
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Trp	Trp	Glu	Phe	Thr	Ala	Ser	Tyr	Asp	Thr	Thr	Cys	Ile	Gly	Leu	
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Ala	Ser	Arg	Pro	Tyr	Ala	Phe	Leu	Glu	Phe	Asp	Ser	Ile	Ile	Gln	
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Lys	Val	Lys	Trp	His	Phe	Asn	Tyr	Val	Ser	Ser	Ser	Gln	Met	Glu	
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Cys	Ser	Leu	Glu	Lys	Ile	Gln	Glu	Glu	Leu	Lys	Leu	Gln	Pro	Pro	
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<213> Homo sapiens

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gaggaggagg cttcagccat cagcaataaa gttgatccca gggaaaaaaa 2300

<210> 138  
<211> 489  
<212> PRT  
<213> Homo sapiens

<400> 138  
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Ala Thr Leu Tyr Ile Leu Cys His Ile Phe Leu Thr Arg Phe Lys  
35 40 45  
Lys Pro Ala Glu Phe Thr Thr Val Asp Asp Glu Asp Ala Thr Val  
50 55 60  
Asn Lys Ile Ala Leu Glu Leu Cys Thr Phe Thr Leu Ala Ile Ala  
65 70 75  
Leu Gly Ala Val Leu Leu Leu Pro Phe Ser Ile Ile Ser Asn Glu  
80 85 90  
Val Leu Leu Ser Leu Pro Arg Asn Tyr Tyr Ile Gln Trp Leu Asn  
95 100 105  
Gly Ser Leu Ile His Gly Leu Trp Asn Leu Val Phe Leu Phe Pro  
110 115 120  
Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala Tyr Phe Phe Thr

				125					130					135
Glu	Ser	Glu	Gly	Phe 140	Ala	Gly	Ser	Arg	Lys 145	Gly	Val	Leu	Gly	Arg 150
Val	Tyr	Glu	Thr	Val 155	Val	Met	Leu	Met	Leu 160	Leu	Thr	Leu	Leu	Val 165
Leu	Gly	Met	Val	Trp 170	Val	Ala	Ser	Ala	Ile 175	Val	Asp	Lys	Asn	Lys 180
Ala	Asn	Arg	Glu	Ser 185	Leu	Tyr	Asp	Phe	Trp 190	Glu	Tyr	Tyr	Leu	Pro 195
Tyr	Leu	Tyr	Ser	Cys 200	Ile	Ser	Phe	Leu	Gly 205	Val	Leu	Leu	Leu	Leu 210
Val	Cys	Thr	Pro	Leu 215	Gly	Leu	Ala	Arg	Met 220	Phe	Ser	Val	Thr	Gly 225
Lys	Leu	Leu	Val	Lys 230	Pro	Arg	Leu	Leu	Glu 235	Asp	Leu	Glu	Glu	Gln 240
Leu	Tyr	Cys	Ser	Ala 245	Phe	Glu	Glu	Ala	Ala 250	Leu	Thr	Arg	Arg	Ile 255
Cys	Asn	Pro	Thr	Ser 260	Cys	Trp	Leu	Pro	Leu 265	Asp	Met	Glu	Leu	Leu 270
His	Arg	Gln	Val	Leu 275	Ala	Leu	Gln	Thr	Gln 280	Arg	Val	Leu	Leu	Glu 285
Lys	Arg	Arg	Lys	Ala 290	Ser	Ala	Trp	Gln	Arg 295	Asn	Leu	Gly	Tyr	Pro 300
Leu	Ala	Met	Leu	Cys 305	Leu	Leu	Val	Leu	Thr 310	Gly	Leu	Ser	Val	Leu 315
Ile	Val	Ala	Ile	His 320	Ile	Leu	Glu	Leu	Leu 325	Ile	Asp	Glu	Ala	Ala 330
Met	Pro	Arg	Gly	Met 335	Gln	Gly	Thr	Ser	Leu 340	Gly	Gln	Val	Ser	Phe 345
Ser	Lys	Leu	Gly	Ser 350	Phe	Gly	Ala	Val	Ile 355	Gln	Val	Val	Leu	Ile 360
Phe	Tyr	Leu	Met	Val 365	Ser	Ser	Val	Val	Gly 370	Phe	Tyr	Ser	Ser	Pro 375
Leu	Phe	Arg	Ser	Leu 380	Arg	Pro	Arg	Trp	His 385	Asp	Thr	Ala	Met	Thr 390
Gln	Ile	Ile	Gly	Asn 395	Cys	Val	Cys	Leu	Leu 400	Val	Leu	Ser	Ser	Ala 405
Leu	Pro	Val	Phe	Ser 410	Arg	Thr	Leu	Gly	Leu 415	Thr	Arg	Phe	Asp	Leu 420
Leu	Gly	Asp	Phe	Gly 425	Arg	Phe	Asn	Trp	Leu 430	Gly	Asn	Phe	Tyr	Ile 435
Val	Phe	Leu	Tyr	Asn	Ala	Ala	Phe	Ala	Gly	Leu	Thr	Thr	Leu	Cys

440	445	450
Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu Ile Arg		
455	460	465
Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe Pro		
470	475	480
Gln Ala Ser Arg Lys Thr Gln His Gln		
485		

<210> 139  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 53, 57  
 <223> unknown base

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 tcatgctgag cagagtatgg aagcacctga ctacgaagtg ctatccgtgc 150  
 gagaacagct attccacgag aggatccgag agtgtattat atcaacactt 200  
 ctgtttgcaa cactgtacat cctctgccac atcttcctga cccgcttcaa 250  
 gaagcctgct gatttcacca cagtggatga tgaagatgcc accg 294

<210> 140  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 197, 349  
 <223> unknown base

<400> 140  
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 gagccccaga ctgccccgag tttctgtcgc aggcgtgcgag gaaaggcccc 150  
 taggctgggt ctggtgcttg gcggcggcgg cttcctcccc gttgtcntcc 200  
 ccggggcccag aggcacctcg gcttcagtca tgctgagcag agtatggaag 250  
 cacctgacta cgaagtgcta tccgtgcgag aacagctatt ccacgagagg 300  
 atccgcgagt gtattatatc aacactttctg tttgcaaacac tgtacatcnt 350  
 ctgccacatc ttcctgacct gcttcaagaa gcctgctgag ttcaccacag 400  
 tggatgatga agatgccacc gtcaacaaga ttgcgctcga gctgtgcacc 450







gaggaacccat ggctccgcag aacctgagca ccttttgcct gttgctgcta 200  
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 ggtgcctcga agtgccctcta taaaggatat taaaaaggcc tataggaaac 300  
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 gagaaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400  
 gaaacggaaa cagtacgata cttatggtga agaaggatta aaagatggtc 450  
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 ccctggggcgc ttccaaatga cccaggaggt ggtctgcgac gaatgcccta 750  
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 tcattagtig agtcactggt tggctttgag atggatatta ctcaattgga 1000  
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 aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200  
 tgcagaaggt atacaatgga ctgcaaggat attgagagtg aataaaattg 1250  
 gactttgttt aaaataagtg aataagcgat atttattatc tgcaagggtt 1300  
 ttttgtgtgt gtttttgttt ttattttcaa tatgcaagtt aggtttaatt 1350  
 tttttatcta atgatcatca tgaaatgaat aagagggtt aagaatttgt 1400  
 ccatttgcac tcggaaaaga atgaccagca aaagggttac taatacctct 1450  
 ccctttgggg atttaatgtc tgggtgctgcc gcctgagttt caagaattaa 1500  
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<210> 148  
 <211> 358  
 <212> PRT

[illegible]

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Leu	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile	Leu
				20					25					30
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr
				35					40					45
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp
				50					55					60
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu
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Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly
				80					85					90
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile
				95					100					105
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr
				110					115					120
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile	Ile
				125					130					135
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn	Phe
				140					145					150
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro	Gly
				155					160					165
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln	Leu
				170					175					180
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu
				185					190					195
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val
				200					205					210
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile
				215					220					225
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
				230					235					240
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly
				245					250					255
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu
				260					265					270
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val
				275					280					285
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp
				290					295					300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys  
305 310 315

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln  
320 325 330

Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln  
335 340 345

Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr  
350 355

<210> 149

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,  
482

<223> unknown base

<400> 149

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gaccgggaca gaggaaccat ggttccgcag aacntgagca cnttttgcct 150

gttgntgnta tacttcatcg gggcggtgat tgccggacga gatttntata 200

agattttggg gtgcctngaa gtgccttnta taaaggatat taaaaaggcc 250

tataggaaac tagccctgca gntttatccc gaccggaacc ctgatgatcc 300

acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350

cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400

aaagatggtn atcagagctc ccatggagac attttttcac acttntttgg 450

ggattttggt ttcattgtttg gaggaacccc tngtcagcaa gacagaaata 500

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<210> 150

<211> 1532

<212> DNA

<213> Homo sapiens

<400> 150

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ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150

gaccgggact gagtcaggag ccctctggaa gcatggagac tgtggtgatt 200

gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250

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gagatccccg tcagtttatg cctcttttgc agttgcaaac tgtggctggt 1050  
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agaggagtat tgaaaactgg tggactgtca gctttattta gctcacctag 1150  
tgttttcaag aaaattgagc caccgtctaa gaaatcaaga ggtttcacat 1200  
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<210> 151

<211> 226

<212> PRT

<213> Homo sapiens

<400> 151

Met	Glu	Thr	Val	Val	Ile	Val	Ala	Ile	Gly	Val	Leu	Ala	Thr	Ile
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Phe	Leu	Ala	Ser	Phe	Ala	Ala	Leu	Val	Leu	Val	Cys	Arg	Gln	Arg
				20					25					30

Tyr	Cys	Arg	Pro	Arg	Asp	Leu	Leu	Gln	Arg	Tyr	Asp	Ser	Lys	Pro
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[illegible]

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<210> 152
<211> 1027
<212> DNA
<213> Homo sapiens
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<220>  
<221> unsure  
<222> 1017, 1020  
<223> unknown base
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aaaattggaa tgggattaac aggatttggg gtgtttttcc tgttccttgg 150
aatgattctc ttttttgaca aagcactact ggctattgga aatgttttat 200
ttgtagccgg cttggctttt gtaattggtt tagaaagaac attcagattc 250
ttcttccaaa aacataaaat gaaagctaca ggtttttttc tgggtggtgt 300
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 attagaagag tgccagtcct tggatccctc ctaaatttac ctggaattag 450  
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 tatttccagt tgcactgtat ctctggaagt gatgcatgaa ttcgattgga 950  
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 ggattacttt tttttngncn cagggcc 1027

<210> 153  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> N-myristoylation Sites  
 <222> 11-16, 51-56 and 116-121  
 <223> N-myristoylation Sites.

<220>  
 <221> Transmembrane domains  
 <222> 12-30, 33-52, 69-89 and 93-109  
 <223> Transmembrane domains

<220>  
 <221> Aminoacyl-transfer RNA Synthetases.  
 <222> 49-59  
 <223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153  
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                     20                    25                    30  
 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly  
                     35                    40                    45  
 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe  
                     50                    55                    60





caacaccatt cagctcttca ctctcctcct ctggcccatt aacaagcagc 300  
 tcttccggaa gatcaactgc agactgtcct attgcatctc aagccagctg 350  
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 taaagtgctt ttctgggtca aaaaaaaaaa a 1781

<210> 156





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<210> 158  
 <211> 409  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu  
 1 5 10 15  
 Gly Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu  
 20 25 30  
 Gly Phe Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile  
 35 40 45  
 Thr Asp Ser Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp  
 50 55 60  
 Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn  
 65 70 75  
 Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser  
 80 85 90  
 Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg His  
 95 100 105

Ser	Asp	Gln	Ile	Met	Thr	Phe	Arg	Glu	Arg	Leu	Leu	His	Lys	Asn	110	115	120
Leu	Gln	Glu	His	Phe	Ser	Asn	Gln	Asp	Leu	Val	Phe	Leu	Leu	Leu	125	130	135
Thr	Pro	Ser	Ile	Ile	Thr	Glu	Ser	Cys	Ser	Thr	His	Arg	Leu	Glu	140	145	150
His	Ser	Leu	Tyr	Lys	Pro	Gln	Lys	Gly	Leu	Phe	His	Arg	Val	Pro	155	160	165
Leu	Val	Val	Ala	Asn	Leu	Gly	Met	Ser	Glu	Gln	Leu	Gly	Tyr	Lys	170	175	180
Thr	Val	Ser	Gly	Ser	Cys	Met	Ser	Thr	Gly	Phe	Ser	Arg	Ala	Val	185	190	195
Gln	Thr	His	Ser	Ser	Lys	Phe	Phe	Glu	Glu	Asp	Gly	Ser	Leu	Lys	200	205	210
Glu	Val	His	Lys	Ile	Asn	Glu	Met	Tyr	Ala	Ser	Leu	Gln	Glu	Glu	215	220	225
Leu	Lys	Ser	Ile	Cys	Lys	Lys	Val	Glu	Asp	Ser	Glu	Gln	Ala	Val	230	235	240
Asp	Lys	Leu	Val	Lys	Asp	Val	Asn	Arg	Leu	Lys	Arg	Glu	Ile	Glu	245	250	255
Lys	Arg	Arg	Gly	Ala	Gln	Ile	Gln	Ala	Ala	Arg	Glu	Lys	Asn	Ile	260	265	270
Gln	Lys	Asp	Pro	Gln	Glu	Asn	Ile	Phe	Leu	Cys	Gln	Ala	Leu	Arg	275	280	285
Thr	Phe	Phe	Pro	Asn	Ser	Glu	Phe	Leu	His	Ser	Cys	Val	Met	Ser	290	295	300
Leu	Lys	Asn	Arg	His	Val	Ser	Lys	Ser	Ser	Cys	Asn	Tyr	Asn	His	305	310	315
His	Leu	Asp	Val	Val	Asp	Asn	Leu	Thr	Leu	Met	Val	Glu	His	Thr	320	325	330
Asp	Ile	Pro	Glu	Ala	Ser	Pro	Ala	Ser	Thr	Pro	Gln	Ile	Ile	Lys	335	340	345
His	Lys	Ala	Leu	Asp	Leu	Asp	Asp	Arg	Trp	Gln	Phe	Lys	Arg	Ser	350	355	360
Arg	Leu	Leu	Asp	Thr	Gln	Asp	Lys	Arg	Ser	Lys	Ala	Asn	Thr	Gly	365	370	375
Ser	Ser	Asn	Gln	Asp	Lys	Ala	Ser	Lys	Met	Ser	Ser	Pro	Glu	Thr	380	385	390
Asp	Glu	Glu	Ile	Glu	Lys	Met	Lys	Gly	Phe	Gly	Glu	Tyr	Ser	Arg	395	400	405
Ser	Pro	Thr	Phe														

<210> 159  
<211> 2651  
<212> DNA  
<213> Homo sapiens

<400> 159  
ggcacagccg cgcggcggag ggcagagtca gccgagccga gtccagccgg 50  
acgagcggac cagcgcaggg cagcccaagc agcgcgcagc gaacgccccg 100  
cgccgcccac accctctgcg gtccccgcgg cgcttgccac ccttccctcc 150  
ttccccgcgt ccccgccctcg ccggccagtc agcttgccgg gttcgctgcc 200  
ccgcgaaacc ccgaggtcac cagcccgcgc ctctgcttcc ctgggcccgc 250  
cgccgcctcc acgccctcct tctcccttgg ccggcgccct ggcaaccggg 300  
accgttgccct gacgcgaggg ccagctctac ttttcgcccc gcgtctctcc 350  
cgcttgctcg cctcttccac caactccaac tccttctccc tccagctcca 400  
ctcgctagtc cccgactccg ccagccctcg gcccgctgcc gtagcgccgc 450  
ttcccgctcg gtcccaaagg tgggaacgcg tccgccccgg ccgcacccat 500  
ggcacggttc ggcttgcccg cgcttctctg caccctggca gtgctcagcg 550  
ccgcgctgct ggctgccgag ctcaagtcga aaagttgctc ggaagtgcga 600  
cgtcttttac tgtccaaagg cttcaacaag aacgatgccc ccctccacga 650  
gatcaacggg gatcatttga agatctgtcc ccagggttct acctgctgct 700  
ctcaagagat ggaggagaag tacagcctgc aaagtaaaga tgatttcaaa 750  
agtgtggtca gcgaacagtg caatcatttg caagctgtct ttgcttcacg 800  
ttacaagaag tttgatgaat tcttcaaaga actacttgaa aatgcagaga 850  
aatccctgaa tgatatgttt gtgaagacat atggccattt atacatgcaa 900  
aattctgagc tatttaaaga tctcttcgta gagttgaaac gttactacgt 950  
ggtgggaaat gtgaacctgg aagaaatgct aaatgacttc tgggctcgcc 1000  
tctggagcg gatgttccgc ctggtgaact ccagtagcca ctttacagat 1050  
gagtatctgg aatgtgtgag caagtatacg gagcagctga agcccttcgg 1100  
agatgtccct cgcaaattga agctccaggt tactcgtgct tttgtagcag 1150  
ccgtacttt cgctcaaggc ttagcgggtg cgggagatgt cgtgagcaag 1200  
gtctccgtgg taaaccccac agcccagtggt acccatgccc tgttgaagat 1250  
gatctactgc tcccactgcc ggggtctcgt gactgtgaag ccatgttaca 1300  
actactgctc aaacatcatg agaggctgtt tggccaacca aggggatctc 1350  
gattttgaat ggaacaattt catagatgct atgctgatgg tggcagagag 1400  
gctagagggt cctttcaaca ttgaatcggc catggatccc atcgatgtga 1450

agattttctga tgctattatg aacatgcagg ataatagtgt tcaagtgtct 1500  
 cagaagggttt tccagggatg tggaccccc aagcccctcc cagctggacg 1550  
 aattttctcgt tccatctctg aaagtgcctt cagtgtctcg ttcagaccac 1600  
 atcaccccgga ggaacgcca accacagcag ctggcactag tttggaccga 1650  
 ctggttactg atgtcaagga gaaactgaaa caggccaaga aattctggtc 1700  
 ctcccttccg agcaacgttt gcaacgatga gaggatggct gcaggaaacg 1750  
 gcaatgagga tgactgttgg aatgggaaag gcaaaagcag gtacctgttt 1800  
 gcagtgcag gaaatggatt agccaaccag ggcaacaacc cagaggtcca 1850  
 gggttgacacc agcaaaccag acatactgat ccttcgtcaa atcatggctc 1900  
 ttccagatgat gaccagcaag atgaagaatg catacaatgg gaacgacgtg 1950  
 gactttcttg atatcagtga tgaaagtgt ggagaaggaa gtggaagtgg 2000  
 ctgtgagtat cagcagtgcc cttcagagtt tgactacaat gccactgacc 2050  
 atgctgggaa gagtgccaat gagaaagccg acagtgtctg tgtccgtcct 2100  
 ggggcacagg cctacctcct cactgtcttc tgcactctgt tcctggttat 2150  
 gcagagagag tggagataat tctcaaactc tgagaaaaag tgttcatcaa 2200  
 aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc 2250  
 tttttaaatg aatggacaac aatgtacagt ttttactatg tggccactgg 2300  
 ttttaagaagt gctgactttg ttttctcatt cagttttggg aggaaaaggg 2350  
 actgtgcatt gagttgggtc ctgctcccc aaaccatgtt aaacgtggct 2400  
 aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca 2450  
 ctctattatt tgtttgtatg ttttttctc atttcgtttg tgggtttttt 2500  
 tttccaactg tgatctcgcc ttgtttctta caagcaaacc agggtcctt 2550  
 cttggcacgt aacatgtacg tatttctgaa atattaaata gctgtacaga 2600  
 agcagggtttt atttatcatg ttatcttatt aaaagaaaaa gcccaaaaag 2650

c 2651

<210> 160  
 <211> 556  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val  
 1 5 10 15  
 Leu Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys  
 20 25 30  
 Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn



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	35	40	45
Asp Ala Pro Leu His Glu Ile Asn Gly Asp His Leu Lys Ile Cys	50	55	60
Pro Gln Gly Ser Thr Cys Cys Ser Gln Glu Met Glu Glu Lys Tyr	65	70	75
Ser Leu Gln Ser Lys Asp Asp Phe Lys Ser Val Val Ser Glu Gln	80	85	90
Cys Asn His Leu Gln Ala Val Phe Ala Ser Arg Tyr Lys Lys Phe	95	100	105
Asp Glu Phe Phe Lys Glu Leu Leu Glu Asn Ala Glu Lys Ser Leu	110	115	120
Asn Asp Met Phe Val Lys Thr Tyr Gly His Leu Tyr Met Gln Asn	125	130	135
Ser Glu Leu Phe Lys Asp Leu Phe Val Glu Leu Lys Arg Tyr Tyr	140	145	150
Val Val Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Arg Leu Val Asn Ser Gln Tyr	170	175	180
His Phe Thr Asp Glu Tyr Leu Glu Cys Val Ser Lys Tyr Thr Glu	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Leu Gln	200	205	210
Val Thr Arg Ala Phe Val Ala Ala Arg Thr Phe Ala Gln Gly Leu	215	220	225
Ala Val Ala Gly Asp Val Val Ser Lys Val Ser Val Val Asn Pro	230	235	240
Thr Ala Gln Cys Thr His Ala Leu Leu Lys Met Ile Tyr Cys Ser	245	250	255
His Cys Arg Gly Leu Val Thr Val Lys Pro Cys Tyr Asn Tyr Cys	260	265	270
Ser Asn Ile Met Arg Gly Cys Leu Ala Asn Gln Gly Asp Leu Asp	275	280	285
Phe Glu Trp Asn Asn Phe Ile Asp Ala Met Leu Met Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Asp Ala Ile Met Asn Met Gln Asp Asn Ser	320	325	330
Val Gln Val Ser Gln Lys Val Phe Gln Gly Cys Gly Pro Pro Lys	335	340	345
Pro Leu Pro Ala Gly Arg Ile Ser Arg Ser Ile Ser Glu Ser Ala			

	350		355		360
Phe Ser Ala Arg	Phe Arg Pro His His	Pro Glu Glu Arg Pro Thr			
	365	370			375
Thr Ala Ala Gly	Thr Ser Leu Asp Arg	Leu Val Thr Asp Val Lys			
	380	385			390
Glu Lys Leu Lys	Gln Ala Lys Lys Phe	Trp Ser Ser Leu Pro Ser			
	395	400			405
Asn Val Cys Asn	Asp Glu Arg Met Ala	Ala Gly Asn Gly Asn Glu			
	410	415			420
Asp Asp Cys Trp	Asn Gly Lys Gly Lys	Ser Arg Tyr Leu Phe Ala			
	425	430			435
Val Thr Gly Asn	Gly Leu Ala Asn Gln	Gly Asn Asn Pro Glu Val			
	440	445			450
Gln Val Asp Thr	Ser Lys Pro Asp Ile	Leu Ile Leu Arg Gln Ile			
	455	460			465
Met Ala Leu Arg	Val Met Thr Ser Lys	Met Lys Asn Ala Tyr Asn			
	470	475			480
Gly Asn Asp Val	Asp Phe Phe Asp Ile	Ser Asp Glu Ser Ser Gly			
	485	490			495
Glu Gly Ser Gly	Ser Gly Cys Glu Tyr	Gln Gln Cys Pro Ser Glu			
	500	505			510
Phe Asp Tyr Asn	Ala Thr Asp His Ala	Gly Lys Ser Ala Asn Glu			
	515	520			525
Lys Ala Asp Ser	Ala Gly Val Arg Pro	Gly Ala Gln Ala Tyr Leu			
	530	535			540
Leu Thr Val Phe	Cys Ile Leu Phe Leu	Val Met Gln Arg Glu Trp			
	545	550			555

Arg

<210> 161  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 161  
 ctccgtggtgta aacccacag ccc 23

<210> 162  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 162  
tcacatcgat gggatccatg accg 24

<210> 163  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 163  
ggtctcgtga ctgtgaagcc atgttacaac tactgctcaa acatcatgag 50

<210> 164  
<211> 870  
<212> DNA  
<213> Homo sapiens

<400> 164  
ctcgccctca aatgggaacg ctggcctggg actaaagcat agaccaccag 50  
gctgagtatc ctgacctgag tcatccccag ggatcaggag cctccagcag 100  
ggaaccttcc attatattct tcaagcaact tacagctgca cgcacagttg 150  
cgatgaaagt tctaattctt tccctcctcc tgttgctgcc actaatgctg 200  
atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag 250  
ggaccgaggc caggcttcta ggagatggct ccaggaaggc ggccaagaat 300  
gtgagtgcaa agattggttc ctgagagccc cgagaagaaa attcatgaca 350  
gtgtctgggc tgccaaagaa gcagtgtccc tgtgatcatt tcaagggcaa 400  
tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt 450  
ccagagcctg ccagcaattt ctcaaacaat gtcagctaag aagctttgct 500  
ctgcctttgt aggagctctg agcgcccact cttccaatta aacattctca 550  
gccaaagaaga cagtgagcac acctaccaga cactcttctt ctcccacctc 600  
actctcccac tgtaccaccc cctaaatcat tccagtgtc tcaaaaagca 650  
tgtttttcaa gatcattttg tttgttgctc tctctagtgt cttcttctct 700  
cgtcagtctt agcctgtgcc ctccccttac ccaggcttag gcttaattac 750  
ctgaaagatt ccaggaaact gtagcttcct agctagtgtc atttaacctt 800  
aaatgcaatc aggaaagtag caaacagaag tcaataaata tttttaaatg 850  
tcaaaaaaaaa aaaaaaaaaa 870

<210> 165  
<211> 119  
<212> PRT  
<213> Homo sapiens

<400> 165  
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met



	20		25		30
Asp Asp Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe					
	35		40		45
Pro Lys Phe Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala					
	50		55		60
Val Glu Phe Ile Leu Arg Ser Met Ser Arg Ser Thr Gly Phe Met					
	65		70		75
Glu Phe Asp Asp Asn Glu Gly Lys His Ser Ser Lys					
	80		85		

<210> 168  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

<400> 168  
 ggacgccagc gcctgcagag gctgagcagg gaaaaagcca gtgccccagc 50  
 ggaagcacag ctacagagctg gtctgccatg gacatcctgg tcccactcct 100  
 gcagctgctg gtgctgcttc ttaccctgcc cctgcacctc atggctctgc 150  
 tgggctgctg gcagccccctg tgcaaaagct acttccccta cctgatggcc 200  
 gtgctgactc ccaagagcaa ccgcaagatg gagagcaaga aacgggagct 250  
 cttcagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac 300  
 tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc 350  
 tgcagggtca cctgcctaga cccaaatccc cactttgaga agttcctgac 400  
 aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtgg 450  
 ctccctggaga ggacatgaga cagctggctg atggctccat ggatgtggtg 500  
 gtctgcactc tgggtgctgtg ctctgtgcag agcccaagga aggtcctgca 550  
 ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc 600  
 atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc 650  
 gagcccacct ggaaacacat tggggatggc tgctgcctca ccagagagac 700  
 ctggaaggat cttgagaacg ccagtttctc cgaaatccaa atggaacgac 750  
 agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag 800  
 gctgtcaaac aatctttccc aagctccaag gcactcattt gtccttccc 850  
 cagcctccaa ttagaacaag ccacccacca gcctatctat cttccactga 900  
 gagggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc 950  
 ctctctcccc aacctctgcc agggcaatct ctaacttcaa tccgccttc 1000  
 gacagtgaaa aagctctact tctacgctga cccaggaggg aaacactagg 1050  
 accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt 1100



Pro	Pro	Pro	Leu	Lys	Trp	Leu	Pro	Val	Gly	Pro	His	Ile	Met	Gly
				230					235					240
Lys	Ala	Val	Lys	Gln	Ser	Phe	Pro	Ser	Ser	Lys	Ala	Leu	Ile	Cys
				245					250					255
Ser	Phe	Pro	Ser	Leu	Gln	Leu	Glu	Gln	Ala	Thr	His	Gln	Pro	Ile
				260					265					270
Tyr	Leu	Pro	Leu	Arg	Gly	Thr								
				275										

<210> 170  
 <211> 1621  
 <212> DNA  
 <213> Homo sapiens

<400> 170  
 gtgggatttta tttgagtgc aagatcgtttt ctcagtgggtg gtggaagtgtg 50  
 cctcatcgca ggcagatgtt ggggctttgt ccgaacagct cccctctgcc 100  
 agcttctgtgata gataaggggtt aaaaactaat atttatatga cagaagaaaa 150  
 agatgtcatt ccgtaaagta aacatcatca tcttggtcct ggctgttgct 200  
 ctcttcttac tggttttgca ccataacttc ctcagcttga gcagtttgtt 250  
 aaggaatgag gttacagatt caggaattgt agggcctcaa cctatagact 300  
 ttgtcccaaa tgctctccga catgcagtag atgggagaca agaggagatt 350  
 cctgtggtca tcgctgcac tgaagacagg cttggggggg ccattgcagc 400  
 tataaacagc attcagcaca aactcgctc caatgtgatt ttctacattg 450  
 ttactctcaa caatacagca gaccatctcc ggtcctggct caacagtgat 500  
 tccctgaaaa gcatcagata caaaattgtc aattttgacc ctaaactttt 550  
 ggaaggaaaa gttaaaggagg atcctgacca gggggaatcc atgaaacctt 600  
 taacctttgc aaggtttctac ttgccaatcc tggttcccag cgcaaagaag 650  
 gccatataca tggatgatga tgtaattgtg caaggtgata ttcttgccct 700  
 ttacaataca gcactgaagc caggacatgc agctgcattt tcagaagatt 750  
 gtgattcagc ctctactaaa gttgtcatcc gtggagcagg aaaccagtac 800  
 aattacattg gctatcttga ctataaaaag gaaagaattc gtaagctttc 850  
 catgaaagcc agcacttgct catttaaatcc tggagttttt gttgcaaacc 900  
 tgacggaatg gaaacgacag aatataacta accaactgga aaaatggatg 950  
 aaactcaatg tagaagaggg actgtatagc agaaccctgg ctggtagcat 1000  
 cacaacacct cctctgttta tcgtatttta tcaacagcac tctaccatcg 1050  
 atcctatgtg gaatgtccgc caccttggtt ccagtgtctg aaaacgatat 1100  
 tcacctcagt ttgtaaaggc tgccaagtta ctccattgga atggacattt 1150

gaagccatgg ggaaggactg cttcatatac tgatgtttgg gaaaaatggt 1200  
 atattccaga cccaacaggc aaattcaacc taatccgaag atataccgag 1250  
 atctcaaaca taaagtgaag cagaatttga actgtaagca agcattttctc 1300  
 aggaagtcct ggaagatagc atgcatggga agtaacagtt gctaggcttc 1350  
 aatgcctatc ggtagcaagc catggaaaaa gatgtgtcag ctaggtaaag 1400  
 atgacaaaact gccctgtctg gcagtcagct tcccagacag actatagact 1450  
 ataaatatgt ctccatctgc cttaccaagt gttttcttac tacaatgctg 1500  
 aatgactgga aagaagaact gatatggcta gttcagctag ctggtacaga 1550  
 taattcaaaa ctgctgttgg ttttaatttt gtaacctgtg gcctgatctg 1600  
 taaataaaac ttacattttt c 1621

<210> 171

<211> 371

<212> PRT

<213> Homo sapiens

<400> 171

Met	Ser	Phe	Arg	Lys	Val	Asn	Ile	Ile	Ile	Leu	Val	Leu	Ala	Val
1				5					10					15

Ala	Leu	Phe	Leu	Leu	Val	Leu	His	His	Asn	Phe	Leu	Ser	Leu	Ser
				20					25					30

Ser	Leu	Leu	Arg	Asn	Glu	Val	Thr	Asp	Ser	Gly	Ile	Val	Gly	Pro
				35					40					45

Gln	Pro	Ile	Asp	Phe	Val	Pro	Asn	Ala	Leu	Arg	His	Ala	Val	Asp
				50					55					60

Gly	Arg	Gln	Glu	Glu	Ile	Pro	Val	Val	Ile	Ala	Ala	Ser	Glu	Asp
				65					70					75

Arg	Leu	Gly	Gly	Ala	Ile	Ala	Ala	Ile	Asn	Ser	Ile	Gln	His	Asn
				80					85					90

Thr	Arg	Ser	Asn	Val	Ile	Phe	Tyr	Ile	Val	Thr	Leu	Asn	Asn	Thr
				95					100					105

Ala	Asp	His	Leu	Arg	Ser	Trp	Leu	Asn	Ser	Asp	Ser	Leu	Lys	Ser
				110					115					120

Ile	Arg	Tyr	Lys	Ile	Val	Asn	Phe	Asp	Pro	Lys	Leu	Leu	Glu	Gly
				125					130					135

Lys	Val	Lys	Glu	Asp	Pro	Asp	Gln	Gly	Glu	Ser	Met	Lys	Pro	Leu
				140					145					150

Thr	Phe	Ala	Arg	Phe	Tyr	Leu	Pro	Ile	Leu	Val	Pro	Ser	Ala	Lys
				155					160					165

Lys	Ala	Ile	Tyr	Met	Asp	Asp	Asp	Val	Ile	Val	Gln	Gly	Asp	Ile
				170					175					180

Leu	Ala	Leu	Tyr	Asn	Thr	Ala	Leu	Lys	Pro	Gly	His	Ala	Ala	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



185					190					195				
Phe	Ser	Glu	Asp	Cys	Asp	Ser	Ala	Ser	Thr	Lys	Val	Val	Ile	Arg
				200					205					210
Gly	Ala	Gly	Asn	Gln	Tyr	Asn	Tyr	Ile	Gly	Tyr	Leu	Asp	Tyr	Lys
				215					220					225
Lys	Glu	Arg	Ile	Arg	Lys	Leu	Ser	Met	Lys	Ala	Ser	Thr	Cys	Ser
				230					235					240
Phe	Asn	Pro	Gly	Val	Phe	Val	Ala	Asn	Leu	Thr	Glu	Trp	Lys	Arg
				245					250					255
Gln	Asn	Ile	Thr	Asn	Gln	Leu	Glu	Lys	Trp	Met	Lys	Leu	Asn	Val
				260					265					270
Glu	Glu	Gly	Leu	Tyr	Ser	Arg	Thr	Leu	Ala	Gly	Ser	Ile	Thr	Thr
				275					280					285
Pro	Pro	Leu	Leu	Ile	Val	Phe	Tyr	Gln	Gln	His	Ser	Thr	Ile	Asp
				290					295					300
Pro	Met	Trp	Asn	Val	Arg	His	Leu	Gly	Ser	Ser	Ala	Gly	Lys	Arg
				305					310					315
Tyr	Ser	Pro	Gln	Phe	Val	Lys	Ala	Ala	Lys	Leu	Leu	His	Trp	Asn
				320					325					330
Gly	His	Leu	Lys	Pro	Trp	Gly	Arg	Thr	Ala	Ser	Tyr	Thr	Asp	Val
				335					340					345
Trp	Glu	Lys	Trp	Tyr	Ile	Pro	Asp	Pro	Thr	Gly	Lys	Phe	Asn	Leu
				350					355					360
Ile	Arg	Arg	Tyr	Thr	Glu	Ile	Ser	Asn	Ile	Lys				
				365					370					

<210> 172

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 71, 76, 86, 91, 162, 220, 269, 281

<223> unknown base

<400> 172

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[illegible]

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Leu	Leu	Val	His	Ile 35	Phe	Ile	Ser	Leu	Val 40	Ile	Leu	Gly	Leu	Leu 45
Phe	Val	Cys	Gly	Val 50	Leu	Trp	Trp	Leu	Tyr 55	Tyr	Asp	Tyr	Thr	Asn 60
Asp	Leu	Ser	Ile	Glu 65	Leu	Asp	Thr	Glu	Arg 70	Glu	Asn	Met	Lys	Cys 75
Val	Leu	Gly	Phe	Ala 80	Ile	Val	Ser	Thr	Gly 85	Ile	Thr	Ala	Val	Leu 90
Leu	Val	Leu	Ile	Phe	Val	Leu	Arg	Lys	Arg	Ile	Lys	Leu	Thr	Val

95									100					105	
Glu	Leu	Phe	Gln	Ile 110	Thr	Asn	Lys	Ala	Ile 115	Ser	Ser	Ala	Pro	Phe 120	
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Trp	Val	Leu	Trp	Val 140	Ala	Val	Leu	Leu	Ser 145	Leu	Gly	Thr	Ala	Gly 150	
Ala	Ala	Gln	Val	Met 155	Glu	Gly	Gly	Gln	Val 160	Glu	Tyr	Lys	Pro	Leu 165	
Ser	Gly	Ile	Arg	Tyr 170	Met	Trp	Ser	Tyr	His 175	Leu	Ile	Gly	Leu	Ile 180	
Trp	Thr	Ser	Glu	Phe 185	Ile	Leu	Ala	Cys	Gln 190	Gln	Met	Thr	Ile	Ala 195	
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Pro	Asp	His	Pro	Ile 215	Leu	Ser	Ser	Leu	Ser 220	Ile	Leu	Phe	Phe	Tyr 225	
His	Gln	Gly	Thr	Val 230	Val	Lys	Gly	Ser	Phe 235	Leu	Ile	Ser	Val	Val 240	
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Glu	Gln	Gln	His	Gly 260	Ala	Leu	Ser	Arg	Tyr 265	Leu	Phe	Arg	Cys	Cys 270	
Tyr	Cys	Cys	Phe	Trp 275	Cys	Leu	Asp	Lys	Tyr 280	Leu	Leu	His	Leu	Asn 285	
Gln	Asn	Ala	Tyr	Thr 290	Thr	Thr	Ala	Ile	Asn 295	Gly	Thr	Asp	Phe	Cys 300	
Thr	Ser	Ala	Lys	Asp 305	Ala	Phe	Lys	Ile	Leu 310	Ser	Lys	Asn	Ser	Ser 315	
His	Phe	Thr	Ser	Ile 320	Asn	Cys	Phe	Gly	Asp 325	Phe	Ile	Ile	Phe	Leu 330	
Gly	Lys	Val	Leu	Val 335	Val	Cys	Phe	Thr	Val 340	Phe	Gly	Gly	Leu	Met 345	
Ala	Phe	Asn	Tyr	Asn 350	Arg	Ala	Phe	Gln	Val 355	Trp	Ala	Val	Pro	Leu 360	
Leu	Leu	Val	Ala	Phe 365	Phe	Ala	Tyr	Leu	Val 370	Ala	His	Ser	Phe	Leu 375	
Ser	Val	Phe	Glu	Thr 380	Val	Leu	Asp	Ala	Leu 385	Phe	Leu	Cys	Phe	Ala 390	
Val	Asp	Leu	Glu	Thr 395	Asn	Asp	Gly	Ser	Ser 400	Glu	Lys	Pro	Tyr	Phe 405	
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<212> DNA

<213> Homo sapiens

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Table 1. *Continued*

Variable	Mean	SD	Median	Mode	Range	Skewness	Kurtosis
Age	34.2	10.5	32.0	30.0	18-55	0.15	-0.10
Gender	1.0	0.0	1.0	1.0	1-1	0.00	0.00
Marital status	1.0	0.0	1.0	1.0	1-1	0.00	0.00
Education	12.5	1.5	12.0	12.0	10-15	0.10	-0.05
Income	1.5	0.5	1.0	1.0	1-2	0.10	-0.05
Occupation	1.0	0.0	1.0	1.0	1-1	0.00	0.00
Religion	1.0	0.0	1.0	1.0	1-1	0.00	0.00
Health status	1.0	0.0	1.0	1.0	1-1	0.00	0.00
Stress level	2.5	0.5	2.0	2.0	1-3	0.10	-0.05
Life satisfaction	3.5	0.5	3.0	3.0	1-4	0.10	-0.05
Work satisfaction	3.0	0.5	2.5	2.5	1-4	0.10	-0.05
Family satisfaction	3.0	0.5	2.5	2.5	1-4	0.10	-0.05
Community satisfaction	3.0	0.5	2.5	2.5	1-4	0.10	-0.05
Overall satisfaction	3.0	0.5	2.5	2.5	1-4	0.10	-0.05

Met	Arg	Thr	Val	Val	Leu	Thr	Met	Lys	Ala	Ser	Val	Ile	Glu	Met
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Phe	Leu	Val	Leu	Leu	Val	Thr	Gly	Val	His	Ser	Asn	Lys	Glu	Thr
				20					25					30
Ala	Lys	Lys	Ile	Lys	Arg	Pro	Lys	Phe	Thr	Val	Pro	Gln	Ile	Asn
				35					40					45
Cys	Asp	Val	Lys	Ala	Gly	Lys	Ile	Ile	Asp	Pro	Glu	Phe	Ile	Val
				50					55					60
Lys	Cys	Pro	Ala	Gly	Cys	Gln	Asp	Pro	Lys	Tyr	His	Val	Tyr	Gly
				65					70					75
Thr	Asp	Val	Tyr	Ala	Ser	Tyr	Ser	Ser	Val	Cys	Gly	Ala	Ala	Val
				80					85					90
His	Ser	Gly	Val	Leu	Asp	Asn	Ser	Gly	Gly	Lys	Ile	Leu	Val	Arg
				95					100					105
Lys	Val	Ala	Gly	Gln	Ser	Gly	Tyr	Lys	Gly	Ser	Tyr	Ser	Asn	Gly
				110					115					120
Val	Gln	Ser	Leu	Ser	Leu	Pro	Arg	Trp	Arg	Glu	Ser	Phe	Ile	Val
				125					130					135
Leu	Glu	Ser	Lys	Pro	Lys	Lys	Gly	Val	Thr	Tyr	Pro	Ser	Ala	Leu
				140					145					150
Thr	Tyr	Ser	Ser	Ser	Lys	Ser	Pro	Ala	Ala	Gln	Ala	Gly	Glu	Thr
				155					160					165
Thr	Lys	Ala	Tyr	Gln	Arg	Pro	Pro	Ile	Pro	Gly	Thr	Thr	Ala	Gln
				170					175					180
Pro	Val	Thr	Leu	Met	Gln	Leu	Leu	Ala	Val	Thr	Val	Ala	Val	Ala
				185					190					195
Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr
				200					205					210
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu
				215					220					225
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg
				230					235					240
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala
				245					250					255
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val
				260					265					270
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu
				275					280					285
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly

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Ser Thr Ser Ile	Gly Lys Arg Arg Phe	Arg Ile Gln Lys Gln	Leu		
	305	310	315		
Leu Ala Asp Val	Ala Gln Ala Leu Asp	Ile Gly Pro Ala Gly	Pro		
	320	325	330		
Leu Met Gly Val	Val Gln Tyr Gly Asp	Asn Pro Ala Thr His	Phe		
	335	340	345		
Asn Leu Lys Thr	His Thr Asn Ser Arg	Asp Leu Lys Thr Ala	Ile		
	350	355	360		
Glu Lys Ile Thr	Gln Arg Gly Gly Leu	Ser Asn Val Gly Arg	Ala		
	365	370	375		
Ile Ser Phe Val	Thr Lys Asn Phe Phe	Ser Lys Ala Asn Gly	Asn		
	380	385	390		
Arg Ser Gly Ala	Pro Asn Val Val Val	Val Met Val Asp Gly	Trp		
	395	400	405		
Pro Thr Asp Lys	Val Glu Glu Ala Ser	Arg Leu Ala Arg Glu	Ser		
	410	415	420		
Gly Ile Asn Ile	Phe Phe Ile Thr Ile	Glu Gly Ala Ala Glu	Asn		
	425	430	435		
Glu Lys Gln Tyr	Val Val Glu Pro Asn	Phe Ala Asn Lys Ala	Val		
	440	445	450		
Cys Arg Thr Asn	Gly Phe Tyr Ser Leu	His Val Gln Ser Trp	Phe		
	455	460	465		
Gly Leu His Lys	Thr Leu Gln Pro Leu	Val Lys Arg Val Cys	Asp		
	470	475	480		
Thr Asp Arg Leu	Ala Cys Ser Lys Thr	Cys Leu Asn Ser Ala	Asp		
	485	490	495		
Ile Gly Phe Val	Ile Asp Gly Ser Ser	Ser Val Gly Thr Gly	Asn		
	500	505	510		
Phe Arg Thr Val	Leu Gln Phe Val Thr	Asn Leu Thr Lys Glu	Phe		
	515	520	525		
Glu Ile Ser Asp	Thr Asp Thr Arg Ile	Gly Ala Val Gln Tyr	Thr		
	530	535	540		
Tyr Glu Gln Arg	Leu Glu Phe Gly Phe	Asp Lys Tyr Ser Ser	Lys		
	545	550	555		
Pro Asp Ile Leu	Asn Ala Ile Lys Arg	Val Gly Tyr Trp Ser	Gly		
	560	565	570		
Gly Thr Ser Thr	Gly Ala Ala Ile Asn	Phe Ala Leu Glu Gln	Leu		
	575	580	585		
Phe Lys Lys Ser	Lys Pro Asn Lys Arg	Lys Leu Met Ile Leu	Ile		
	590	595	600		
Thr Asp Gly Arg	Ser Tyr Asp Asp Val	Arg Ile Pro Ala Met	Ala		







	440		445		450
Cys Gln Arg Leu	Lys Glu Glu Gln Trp	Glu Val Glu Asp Leu	Met		
	455	460	465		
Arg Glu Phe Tyr	Ser Leu Lys Arg Ser	Arg Ser Lys Phe Gln	Lys		
	470	475	480		
Asn Thr Val Ser	Ser Gly Pro Trp Glu	Pro Pro Ala Arg Pro	Gly		
	485	490	495		
Thr Leu Phe Ser	Pro Glu Asn His Asp	Gln Ala Arg Glu Arg	Lys		
	500	505	510		
Pro Ala Lys Gln	Lys Val Pro Leu Leu	Ser Cys Pro Ser Gln	Pro		
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Ser

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 catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100  
 gcttcctggg cgggctctag aacaattcag gcttcgctgc gactcagacc 150  
 tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
 gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctacaaaa 250  
 tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
 tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
 tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
 tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450  
 gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
 ccccagcagc tgggtgtcac tctactgaagg tcttgagtgt gatgtcactg 550  
 atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
 ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
 ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700  
 acctgggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750  
 gcctactgga ggaggagacc tgggtgccgag gaacatgtca aaatggtgag 800  
 gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850

actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
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 actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000  
 cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctggttgcccc 1050  
 gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100  
 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
 ctctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200  
 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
 aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
 gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggttt 1350  
 gtctaacaga aactgactg aggcttaggg gatgtgacct ctagactggg 1400  
 ggctgccact tgctggctga gcaaccctgg gaaaagtgc ttcattccctt 1450  
 cggctcctaag ttttctcctc tgtaatgggg gaattaccta cacacctgct 1500  
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 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgctccttt tttctgttg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggc aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 183  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> Signal peptide  
 <222> 1-29  
 <223> Signal peptide  
 <220>  
 <221> N-glycosylation sites  
 <222> 40-43, 134-137

[illegible]

<223> Tissue factor proteins homology

<223> Transmembrane domain

<223> Integrins alpha chain protein homology

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu  
215 220 225



Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 184  
 <211> 808  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748  
 <223> unknown base

<400> 184  
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 cctttctagc ttcctggccg gctctagaac aattcaggct tcgctgcgac 100  
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200  
 ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtgggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
 gccattctgc ctgccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctggtg ctactcact gaaggtcctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggccca 550  
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600  
 agaaactcaa ccattccttac ccgacctggg atggagatca ccaaagatgg 650  
 ottncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgacccac 808

<210> 185  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
aggcttcgct gcgactagac ctc 23

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
ccaggtcggg taaggatggt tgag 24

<210> 187  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 188  
<211> 1227  
<212> DNA  
<213> Homo sapiens

<400> 188  
cggaacgctg ggccgccacc tccggaacaa gccatggtgg cggcgacggt 50  
ggcagcggcg tggctgctcc tgtgggctgc ggcctgcgcg cagcaggagc 100  
aggacttcta cgacttcaag gcggtcaaca tccggggcaa actggtgtcg 150  
ctggagaagt accgcggatc ggtgtccctg gtggtgaatg tggccagcga 200  
gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250  
acctgggccc ccaccacttt aacgtgctcg ccttcccctg caaccagttt 300  
ggccaacagg agcctgacag caacaaggag attgagagct ttgcccgccg 350  
cacctacagt gtctcattcc ccatgtttag caagattgca gtcaccggtg 400  
ctggtgccca tcctgccttc aagtacctgg cccagacttc tgggaaggag 450  
cccacctgga acttctggaa gtacctagta gcccagatg gaaaggtggt 500  
aggggcttgg gacccaactg tgtcagtgga ggaggtcaga cccagatca 550  
cagcgctcgt gaggaagctc atcctactga agcgagaaga cttataacca 600

ccgogtctcc tctccacca cctcatcccg cccacctgtg tggggctgac 650  
 caatgcaaac tcaaagtgtg cttcaaaggg agagaccac tgactctcct 700  
 tcttttactc ttatgccatt ggtcccatca ttcttgtggg ggaaaaattc 750  
 tagtattttg attatttgaa tcttacagca acaaatagga actcctggcc 800  
 aatgagagct cttgaccagt gaatcaccag ccgatacgaa cgtcttgcca 850  
 acaaaaatgt gtggcaaata gaagtatatc aagcaataat ctcccacca 900  
 aggcttctgt aaactgggac caatgattac ctcatagggc tgttgtgagg 950  
 attaggatga aatacctgtg aaagtgccta ggcaagtcca gccaaatagg 1000  
 aggcatcaca tgaacatttt ttgcatataa accaaaaaat aacttggtat 1050  
 caataaaaac ttgcatccaa catgaatttc cagccgatga taatccaggc 1100  
 caaaggttta gttgttggtt tttcctctgt attattttct tcattacaaa 1150  
 agaaatgcaa gttcattgta acaatccaaa caatacctca cgatataaaa 1200  
 taaaaatgaa agtatcctcc tcaaaaa 1227

<210> 189

<211> 187

<212> PRT

<213> Homo sapiens

<400> 189

Met	Val	Ala	Ala	Thr	Val	Ala	Ala	Ala	Trp	Leu	Leu	Leu	Trp	Ala	1	5	10	15
Ala	Ala	Cys	Ala	Gln	Gln	Glu	Gln	Asp	Phe	Tyr	Asp	Phe	Lys	Ala	20	25	30	
Val	Asn	Ile	Arg	Gly	Lys	Leu	Val	Ser	Leu	Glu	Lys	Tyr	Arg	Gly	35	40	45	
Ser	Val	Ser	Leu	Val	Val	Asn	Val	Ala	Ser	Glu	Cys	Gly	Phe	Thr	50	55	60	
Asp	Gln	His	Tyr	Arg	Ala	Leu	Gln	Gln	Leu	Gln	Arg	Asp	Leu	Gly	65	70	75	
Pro	His	His	Phe	Asn	Val	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly	80	85	90	
Gln	Gln	Glu	Pro	Asp	Ser	Asn	Lys	Glu	Ile	Glu	Ser	Phe	Ala	Arg	95	100	105	
Arg	Thr	Tyr	Ser	Val	Ser	Phe	Pro	Met	Phe	Ser	Lys	Ile	Ala	Val	110	115	120	
Thr	Gly	Thr	Gly	Ala	His	Pro	Ala	Phe	Lys	Tyr	Leu	Ala	Gln	Thr	125	130	135	
Ser	Gly	Lys	Glu	Pro	Thr	Trp	Asn	Phe	Trp	Lys	Tyr	Leu	Val	Ala	140	145	150	
Pro	Asp	Gly	Lys	Val	Val	Gly	Ala	Trp	Asp	Pro	Thr	Val	Ser	Val				

	155		160		165
Glu Glu Val Arg	Pro Gln Ile Thr Ala	Leu Val Arg Lys Leu	Ile		
	170	175	180		
Leu Leu Lys Arg	Glu Asp Leu				
	185				

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 190  
 gcagacttc tacgacttca aggc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 191  
 agtctgggcc aggtacttga aggc 24

<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 192  
 caacatccgg ggcaactgg tgctgctgga gaagtaccgc ggatcgggtgt 50

<210> 193  
 <211> 2187  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 cggacgcgtg ggcgggcccgg gacgcagggc aaagcgagcc atggctgtct 50  
 acgtcgggat gctgcgcctg gggaggctgt gcgccgggag ctcgggggtg 100  
 ctggggggccc gggccgccct ctctcgaggt tggcaggaag ccaggttgca 150  
 ggggtgtccgc ttcctcagtt ccagagaggt ggatcgcgat gtctccacgc 200  
 ccatcggagg cctcagctac gttcaggggt gcacaaaaaa gcatcttaac 250  
 agcaagactg tgggccagtg cctggagacc acagcacaga ggggtcccaga 300  
 acgagaggcc ttggtcgtcc tccatgaaga cgtcagggtg acctttgccc 350  
 aactcaagga ggaggtggac aaagctgctt ctggcctcct gagcattggc 400

ctctgcaaag gtgaccggct gggcatgtgg ggacctaact cctatgcatg 450  
 ggtgctcatg cagttggcca ccgcccaggc gggcatcatt ctggtgtctg 500  
 tgaacccagc ctaccaggct atggaactgg agtatgtcct caagaagggtg 550  
 ggctgcaagg cccttgtgtt cccaagcaa ttcaagacct agcaatacta 600  
 caacgtcctg aagcagatct gtccagaagt ggagaatgcc cagccagggg 650  
 ccttgaagag tcagaggctc ccagatctga ccacagtcac ctcggtggat 700  
 gcccctttgc cggggaccct gtcctggat gaagtgggtg cggctggcag 750  
 cacacggcag catctggacc agtccaata caaccagcag ttctgtcct 800  
 gccatgacct catcaacatc cagttcacct cggggacaac aggcagcccc 850  
 aagggggcca ccctctcca ctacaacatt gtcaacaact ccaacatttt 900  
 aggagagcgc ctgaaactgc atgagaagac accagagcag ttgcggatga 950  
 tcctgcccaa cccctgtac cattgcctgg gttccgtggc aggcacaatg 1000  
 atgtgtctga tgtacgggtg caccctcatc ctggcctctc ccatcttcaa 1050  
 tggcaagaag gcaactggagg ccatcagcag agagagaggc accttcctgt 1100  
 atggtacccc cacgatgttc gtggacattc tgaaccagcc agacttctcc 1150  
 agttatgaca tctcgaccat gtgtggaggt gtcattgctg ggtcccctgc 1200  
 acctccagag ttgatccgag ccatcatcaa caagataaat atgaaggacc 1250  
 tgggtggttg ttatggaacc acagagaaca gtcccgtgac attcgcgcac 1300  
 ttccctgagg aactgtgga gcagaaggca gaaagcgtgg gcagaattat 1350  
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 agctgaacac gccgggggag ctgtgcatcc gagggtagtg cgtcatgctg 1450  
 ggctactggg gtgagcctca gaagacagag gaagcagtgg atcaggacaa 1500  
 gtggtattgg acaggagatg tcgccacaat gaatgagcag ggcttctgca 1550  
 agatcgtggg ccgctctaag gatatgatca tccgggggtg tgagaacatc 1600  
 taccgccgag agctcgagga cttctttcac acacacccga aggtgcagga 1650  
 agtgcagggt gtgggagtga aggacgatcg gatgggggaa gagatttgtg 1700  
 cctgcattcg gctgaaggac ggggaggaga ccacggtgga ggagataaaa 1750  
 gctttctgca aagggaagat ctctcacttc aagattccga agtacatcgt 1800  
 gtttgtcaca aactaccccc tcaccatttc aggaaagatc cagaaattca 1850  
 aacttcgaga gcagatggaa cgacatctaa atctgtgaat aaagcagcag 1900  
 gcctgtcctg gccggttggc ttgactctct cctgtcagaa tgcaacctgg 1950  
 ctttatgcac ctagatgtcc ccagcaccca gttctgagcc aggcacatca 2000

aatgtcaagg aattgactga acgaactaag agctcctgga tgggtccggg 2050  
aactgcctg ggcacaagggt gccaaaaggc aggcagcctg cccaggccct 2100  
ccctcctgtc catccccac attcccctgt ctgtccttgt gatttgcat 2150  
aaagagcttc tgttttcttt gaaaaaaaaa aaaaaaa 2187

<210> 194  
<211> 615  
<212> PRT  
<213> Homo sapiens

<400> 194  
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala  
1 5 10 15  
Gly Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser  
20 25 30  
Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg  
35 40 45  
Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr  
50 55 60  
Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly  
65 70 75  
Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala  
80 85 90  
Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu  
95 100 105  
Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly  
110 115 120  
Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Tyr  
125 130 135  
Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile  
140 145 150  
Leu Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr  
155 160 165  
Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln  
170 175 180  
Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro  
185 190 195  
Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu  
200 205 210  
Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly  
215 220 225  
Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln  
230 235 240  
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His



560	565	570
Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr		
575	580	585
Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile		
590	595	600
Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu		
605	610	615

<210> 195  
 <211> 642  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 caactccaac attttaggag agcgccctgaa actgcatgag aagacaccag 50  
 agcagttgcg gatgatcctg cccaaccccc tgtaccattg cctgggttcc 100  
 gtggcaggca caatgatgtg tctgatgtac ggtgccaccc tcatcctggc 150  
 ctctcccatc ttcaatggca agaaggcact ggaggccatc agcagagaga 200  
 gaggcacctt cctgtatggt acccccacga tgttcgtgga cattctgaac 250  
 cagccagact tctccagtta tgacatctcg accatgtgtg gaggtgtcat 300  
 tgctgggtcc cctgcacctc cagagttgat ccgagccatc atcaacaaga 350  
 taaatatgaa ggacctggtg gttgcttatg gaaccacaga gaacagtccc 400  
 gtgacattcg cgcacttccc tgaggacact gtggagcaga aggcagaaag 450  
 cgtgggcaga attatgcctc acacggaggc gcggatcatg aacatggagg 500  
 cagggacgct ggcaaagctg aacacgcccg gggagctgtg catccgaggg 550  
 tactgcgta tgctgggcta ctggggtgag cctcagaaga cagaggaagc 600  
 agtggatcag gacaagtggg attggacagg agatgtcgcc ac 642

<210> 196  
 <211> 1575  
 <212> DNA  
 <213> Homo sapiens

<400> 196  
 gagcaggacg gagccatgga ccccgccagg aaagcaggtg cccaggccat 50  
 gatctggact gcaggctggc tgctgctgct gctgcttcgc ggaggagcgc 100  
 aggccctgga gtgctacagc tgcgtgcaga aagcagatga cggatgctcc 150  
 ccgaacaaga tgaagacagt gaagtgcgcg ccgggcgtgg acgtctgcac 200  
 cgaggccgtg ggggcggtgg agaccatcca cggacaattc tcgctggcag 250  
 tgogggggtt cggttcggga ctccccggca agaataaccg cggcctggat 300  
 cttcacgggc ttctggcggt catccagctg cagcaatgcg ctcaggatcg 350



ctgcaacgcc aagctcaacc tcaectcgcg ggcgctcgac ccggcaggta 400  
atgagagtgc ataccgccc aacggcgtgg agtgctacag ctgtgtgggc 450  
ctgagccggg aggcgtgcca gggtagatcg ccgccggtcg tgagctgcta 500  
caacgccagc gatcatgtct acaagggctg cttegacggc aacgtcacct 550  
tgacggcagc taatgtgact gtgtccttgc ctgtccgggg ctgtgtccag 600  
gatgaattct gcactcggga tggagtaaca ggcccagggt tcacgctcag 650  
tggctcctgt tgccaggggt cccgctgtaa ctctgacctc cgcaacaaga 700  
cctacttctc ccctcgaatc ccaccccttg tccggctgcc ccctccagag 750  
cccacgactg tggcctcaac cacatctgtc accacttcta cctcggcccc 800  
agtgagaccc acatccacca ccaaaccat gccagcgcca accagtcaga 850  
ctccgagaca gggagtagaa cacgaggcct cccgggatga ggagcccagg 900  
ttgactggag ggcgcgctgg ccaccaggac cgcagcaatt cagggcagta 950  
tcctgcaaaa ggggggcccc agcagcccca taataaaggc tgtgtggctc 1000  
ccacagctgg attggcagcc cttctgttgg ccgtggctgc tgggtgtccta 1050  
ctgtgagctt ctccacctgg aaatttccct ctacactact tctctggccc 1100  
tgggtacccc tcttctcatc acttctgtt cccaccactg gactgggctg 1150  
gcccagcccc tgtttttcca acattcccca gtatccccag cttctgtctc 1200  
gctgggttgc ggctttggga aataaaatac cggtgtatat attctgccag 1250  
gggtgttcta gctttttgag gacagctcct gtatccttct catccttgtc 1300  
tctccgcttg tcctcttgtg atgttaggac agagtgcagag aagtcagctg 1350  
tcacggggaa ggtgagagag aggatgctaa gcttcctact cactttctcc 1400  
tagccagcct ggactttgga gcgtgggggt ggtgggacaa tggctcccca 1450  
ctctaagcac tgcctcccct actccccga tctttgggga atcggttccc 1500  
catatgtctt ccttactaga ctgtgagctc ctcgaggggg ggcccggtag 1550  
ccaattcgcc ctatagtgcg tcgta 1575

<210> 197  
<211> 346  
<212> PRT  
<213> Homo sapiens

<400> 197  
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr  
1 5 10 15  
Ala Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala  
20 25 30  
Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser

	35	40	45
Pro Asn Lys Met	Lys Thr Val Lys Cys Ala	Pro Gly Val Asp Val	
	50	55	60
Cys Thr Glu Ala	Val Gly Ala Val Glu Thr	Ile His Gly Gln Phe	
	65	70	75
Ser Leu Ala Val	Arg Gly Cys Gly Ser	Gly Leu Pro Gly Lys Asn	
	80	85	90
Asp Arg Gly Leu	Asp Leu His Gly Leu	Leu Ala Phe Ile Gln Leu	
	95	100	105
Gln Gln Cys Ala	Gln Asp Arg Cys Asn	Ala Lys Leu Asn Leu Thr	
	110	115	120
Ser Arg Ala Leu	Asp Pro Ala Gly Asn	Glu Ser Ala Tyr Pro Pro	
	125	130	135
Asn Gly Val Glu	Cys Tyr Ser Cys Val	Gly Leu Ser Arg Glu Ala	
	140	145	150
Cys Gln Gly Thr	Ser Pro Pro Val Val	Ser Cys Tyr Asn Ala Ser	
	155	160	165
Asp His Val Tyr	Lys Gly Cys Phe Asp	Gly Asn Val Thr Leu Thr	
	170	175	180
Ala Ala Asn Val	Thr Val Ser Leu Pro	Val Arg Gly Cys Val Gln	
	185	190	195
Asp Glu Phe Cys	Thr Arg Asp Gly Val	Thr Gly Pro Gly Phe Thr	
	200	205	210
Leu Ser Gly Ser	Cys Cys Gln Gly Ser	Arg Cys Asn Ser Asp Leu	
	215	220	225
Arg Asn Lys Thr	Tyr Phe Ser Pro Arg	Ile Pro Pro Leu Val Arg	
	230	235	240
Leu Pro Pro Pro	Glu Pro Thr Thr Val	Ala Ser Thr Thr Ser Val	
	245	250	255
Thr Thr Ser Thr	Ser Ala Pro Val Arg	Pro Thr Ser Thr Thr Lys	
	260	265	270
Pro Met Pro Ala	Pro Thr Ser Gln Thr	Pro Arg Gln Gly Val Glu	
	275	280	285
His Glu Ala Ser	Arg Asp Glu Glu Pro	Arg Leu Thr Gly Gly Ala	
	290	295	300
Ala Gly His Gln	Asp Arg Ser Asn Ser	Gly Gln Tyr Pro Ala Lys	
	305	310	315
Gly Gly Pro Gln	Gln Pro His Asn Lys	Gly Cys Val Ala Pro Thr	
	320	325	330
Ala Gly Leu Ala	Ala Leu Leu Leu Ala	Val Ala Ala Gly Val Leu	
	335	340	345
Leu			

<210> 198  
<211> 1657  
<212> DNA  
<213> Homo sapiens

<400> 198

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gtcctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150  
tgattaccag accctgagga ttgggggact ggtgttgcgt gtggtcctct 200  
tctcggttgg gatcctcctt atcctaagtc gcaggtgcaa gtgcagtttc 250  
aatcagaagc cccggggccc aggagatgag gaagcccagg tggagaacct 300  
catcacccgc aatgcaacag agccccagaa gcagagaact gaagtgcagc 350  
catcaggtgg aagcctctgg aacctgaggc ggctgcttga acctttggat 400  
gcaaattgtc atgcttaaga aaaccggcca cttcagcaac agocctttcc 450  
ccaggagaag ccaagaactt gtgtgtcccc caccctatcc cctotaacac 500  
cattcctcca cctgatgatg caactaacac ttgcctcccc actgcagcct 550  
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gtgtgtgttt gctaactgtg gtctttgtgg ctacttggtt gtggatggta 650  
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cacatggcca tctgtctctc cctgcccccg tggccctcca tcacctctg 750  
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acgtcaggca ggctatgcc ttccgtggtt aatttcttcc caggggcttc 1050  
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ttctcagcaa taactccatg ggctctggga ccctaccct tccaaccttc 1200  
cctgcttctg agacttcaat ctacagccca gctcatccag atgcagacta 1250  
cagtccctgc aattgggtct ctggcaggca atagttgaag gactcctgtt 1300  
ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350  
cttctctgcc taogtccct tagatgggca gcagaggcaa ctcccgcac 1400

ctttgctctg cctgtcgggtg gtcagagcgg tgagcgaggt gggttggaga 1450  
ctcagcaggc tccgtgcagc ccttggaac agtgagaggt tgaaggcat 1500  
aacgagagt ggaactcaac ccagatcccc cccctcctgt cctctgtgtt 1550  
cccgcggaac ccaaccaaac cgtgcgctgt gacccattgc tgttctctgt 1600  
atcgtgatct atcctcaaca acaacagaaa aaaggaataa aatatacctt 1650  
gtttcct 1657

<210> 199  
<211> 120  
<212> PRT  
<213> Homo sapiens

<400> 199  
Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met  
1 5 10 15  
Val Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe  
20 25 30  
His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala  
35 40 45  
Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg  
50 55 60  
Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu  
65 70 75  
Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro  
80 85 90  
Gln Lys Gln Arg Thr Glu Val Gln Pro Ser Gly Gly Ser Leu Trp  
95 100 105  
Asn Leu Arg Arg Leu Leu Glu Pro Leu Asp Ala Asn Val Asp Ala  
110 115 120

<210> 200  
<211> 415  
<212> DNA  
<213> Homo sapiens

<400> 200  
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cctcctgggtg ctccactctg ccagaggagc caccctgggt ggtcctgagg 100  
aagaaagcac cattgagaat tatgcgtcac gacccgaggc ctttaacacc 150  
ccgttcctga acatcgacaa attgcgatct gcgtttaagg ctgatgagtt 200  
cctgaactgg cagccctct ttgagtctat caaaaggaaa cttcctttcc 250  
tcaactggga tgcctttcct aagctgaaag gactgaggag cgcaactcct 300  
gatgccagat gaccatgacc tccactggaa gagggggcta gcgtgagcgc 350  
tgattctcaa cctaccataa ctctttcctg cctcaggaac tccaataaaa 400

cattttccat ccaaa 415

<210> 201

<211> 99

<212> PRT

<213> Homo sapiens

<400> 201

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu  
1 5 10 15

Val Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu  
20 25 30

Glu Ser Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn  
35 40 45

Thr Pro Phe Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala  
50 55 60

Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg  
65 70 75

Lys Leu Pro Phe Leu Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly  
80 85 90

Leu Arg Ser Ala Thr Pro Asp Ala Gln  
95

<210> 202

<211> 678

<212> DNA

<213> Homo sapiens

<400> 202

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ggtggagatt gcctttgcct cagtgattct cacctgcctc tcccttcttg 100

cagcaggagt ctcccagggt gttcttctcc agccagttcc aactcaggag 150

acaggtccca aggccatggg agatctctcc tgtggctttg cgggccactc 200

atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250

atgatttaat aaccatcctt tgcgaagttt tatgaggctt taggggaatg 300

tcaacctca aatttttggt atactagatg gcttccattt acccaccact 350

attttaaggt ccctttattt ttaggttcaa gggtcatttg acttgagaaa 400

gtgcocttct gcagcttcat tgattttggt tatcttcaact attaattgta 450

acgattaataa aagaataaga gcacgcagac ctctaggaga atattttatc 500

cctgggtgcc cctgacacat ttatgtagtg atcccacaaa tgtgattggt 550

aatttaaagt ttattctaatt attagtagat tcagttgtga tgtaatatga 600

ataaccagaa tctattttctt aaaagttttg agtatatttt tcaactagat 650

atttgtagat aaagactgaa tagtgatg 678

<210> 203  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Gly Val Glu Ile Ala Phe Ala Ser Val Ile Leu Thr Cys Leu  
 1 5 10 15  
 Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro  
 20 25 30  
 Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser  
 35 40 45  
 Cys Gly Phe Ala Gly His Ser  
 50

<210> 204  
 <211> 1917  
 <212> DNA  
 <213> Homo sapiens

<400> 204  
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 agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150  
 tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200  
 tgggtgcata gaagaggatc taactccttt ccgaggaggc atctccagga 250  
 agatgatggc agaggtagtc agacggaagc tagggacca ctatcagatc 300  
 actaagaaca gactgtaccg ggaaaatgac tgcattgttc cctcaagggtg 350  
 tagtgggtgt gagcacttta ttttggaagt gatcgggcgt ctccctgaca 400  
 tggagatggg gatcaatgta cgagattatc ctcagggttc taaatggatg 450  
 gagcctgcca tccagtcctt ctcttcagtc aagacatcag agtaccatga 500  
 tatcatgtat cctgcttgga cattttggga agggggacct gctgtttggc 550  
 caatttatcc tacaggctct ggacgggtggg acctcttcag agaagatctg 600  
 gtaagggtcag cagcacagtg gccatggaaa aagaaaaact ctacagcata 650  
 tttccgagga tcaaggacaa gtccagaacg agatcctctc attcttctgt 700  
 ctcggaaaaa cccaaaactt gttgatgcag aatacaccaa aaaccaggcc 750  
 tggaaatcta tgaaagatac cttaggaaag ccagctgcta aggatgtcca 800  
 tcttgtggat cactgcaaat acaagtatct gttaattttt cgaggcgtag 850  
 ctgcaagttt ccggttttaa cacctcttcc tgtgtggctc acttgttttc 900  
 catgttggtg atgagtggct agaattcttc tatccacagc tgaagccatg 950  
 ggttcactat atcccagtca aaacagatct ctccaatgtc caagagctgt 1000

tacaatttgt aaaagcaa at gatgatgtag ctcaagagat tgctgaaagg 1050  
 ggaagccagt ttattaggaa ccatttgcag atggatgaca tcacctgtta 1100  
 ctgggagaac ctcttgagt aatactctaa attcctgtct tataatgtaa 1150  
 cgagaaggaa aggttatgat caaattattc ccaaaatggt gaaaactgaa 1200  
 ctatagtagt catcatagga ccatagtcct ctttgtggca acagatctca 1250  
 gatatactac ggtgagaagc ttaccataag cttggctcct ataccttgaa 1300  
 tatctgctat caagccaaat acctggtttt ccttatcatg ctgcacccag 1350  
 agcaactctt gagaaagatt taaaatgtgt ctaatacact gatatgaagc 1400  
 agttcaactt tttggatgaa taaggaccag aaatcgtgag atgtggattt 1450  
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 ggtttctata atgccacata gaaagaggcc aattgcatga gtaattattg 1850  
 caattggatt tcaggttccc tttttgtgcc ttcatgccct acttcttaat 1900  
 gcctctctaa agccaaa 1917

<210> 205  
 <211> 392  
 <212> PRT  
 <213> Homo sapiens

<400> 205  
 Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu  
 1 5 10 15  
 Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser  
 20 25 30  
 Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn  
 35 40 45  
 Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val  
 50 55 60  
 Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys  
 65 70 75  
 Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln  
 80 85 90  
 Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro







[illegible][illegible]

182

<213> Homo sapiens

<400> 208

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gtagttcaca acagatctga gtgttttaat taagcatgga atacagaaaa 150  
caacaaaaaa cttaagcttt aatttcatct ggaattccac agttttctta 200  
gtcccttga cccggttgac ctgttggctc ttcccgtgg ctgctctatc 250  
acgtggtgct ctccgactac tcaccccag tgtaaagaac cttcggctcg 300  
cgtgcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc 350  
gagtaggatg tcaactgagat ccctcaaattg gagcctcctg ctgctgtcac 400  
tcctgagttt ctttgtgatg tggtaacctca gccttcccca ctacaatgtg 450  
atagaacgcg tgaactggat gtacttctat gagtatgagc cgatttacag 500  
acaagacttt cacttcacac ttcgagagca ttcaaactgc tctcatcaaa 550  
atccatttct ggtcattctg gtgacctccc acccttcaga tgtgaaagcc 600  
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tgaggttctt acatttttct tattaggcca agaggctgaa aaggaagaca 700  
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atccgacaag attttttaga cacatataat aacctgacct tgaaaacccat 800  
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tgaagacaga cactgatgtt ttcacataa ctggcaattt agtgaagtat 900  
cttttaaacc taaaccactc agagaagttt ttcacagggt atcctctaata 950  
tgataattat tcctatagag gattttacca aaaaacccat atttcttacc 1000  
aggagtatcc tttcaagggtg ttccctccat actgcagtgg gttgggttat 1050  
ataatgtcca gagatttggg gccaaaggatc tatgaaatga tgggtcacgt 1100  
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taaaagtga cttcatatt ccagaagaca caaatctttt ctttctatat 1200  
agaatccatt tggatgtctg tcaactgaga cgtgtgattg cagcccatgg 1250  
cttttcttcc aaggagatca tcaacttttg gcaggatcatg ctaaggaaca 1300  
ccacatgcc ttattaactt cacattctac aaaaagccta gaaggacagg 1350  
ataccttgtg gaaagtgtta aataaagtag gtactgtgga aaattcatgg 1400  
ggaggtcagt gtgctggctt aactgaact gaaactcatg aaaaaccag 1450  
actggagact ggagggttac acttgtgatt tattagtcag gcccttcaaa 1500

gatgatatgt ggaggaatta aatataaagg aattggaggt ttttgctaaa 1550  
 gaaattaata ggaccaaaca atttggacat gtcattctgt agactagaat 1600  
 ttcttaaaag ggtgttactg agttataagc tcactaggct gtaaaaacaa 1650  
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 aaaaaacttc ttactgaag ttatactgaa caaaatttta cctgtttttg 1800  
 gtcatttata aagtacttca agatgttgca gtatttcaca gttattatta 1850  
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 caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt 1950  
 tacttaactg atcagtttat tattgatata tcactccatt aatgtaaagt 2000  
 cataggtcat tattgcatat cagtaatctc ttggactttg ttaaataattt 2050  
 tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa 2095

<210> 209  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 209  
 Met Ala Ser Ala Leu Trp Thr Val Leu Pro Ser Arg Met Ser Leu  
 1 5 10 15  
 Arg Ser Leu Lys Trp Ser Leu Leu Leu Leu Ser Leu Leu Ser Phe  
 20 25 30  
 Phe Val Met Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu  
 35 40 45  
 Arg Val Asn Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg  
 50 55 60  
 Gln Asp Phe His Phe Thr Leu Arg Glu His Ser Asn Cys Ser His  
 65 70 75  
 Gln Asn Pro Phe Leu Val Ile Leu Val Thr Ser His Pro Ser Asp  
 80 85 90  
 Val Lys Ala Arg Gln Ala Ile Arg Val Thr Trp Gly Glu Lys Lys  
 95 100 105  
 Ser Trp Trp Gly Tyr Glu Val Leu Thr Phe Phe Leu Leu Gly Gln  
 110 115 120  
 Glu Ala Glu Lys Glu Asp Lys Met Leu Ala Leu Ser Leu Glu Asp  
 125 130 135  
 Glu His Leu Leu Tyr Gly Asp Ile Ile Arg Gln Asp Phe Leu Asp  
 140 145 150  
 Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile Met Ala Phe Arg Trp  
 155 160 165



ggacatttcc ttctgtggag acacggtgga gaactaaaca attttttaaa 600  
gccactatgg atttagtcat ctgaatatgc tgtgcagaaa aaatatgggc 650  
tccagtgggtt tttaccatgt cattctgaaa tttttctcta ctagttatgt 700  
ttgatttctt taagtttcaa taaaatcatt tagcattgaa aaaaa 745

<210> 211  
<211> 185  
<212> PRT  
<213> Homo sapiens

<400> 211  
Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu  
1 5 10 15  
Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn  
20 25 30  
Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu  
35 40 45  
His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp  
50 55 60  
Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu  
65 70 75  
Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val  
80 85 90  
Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys  
95 100 105  
Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Pro Lys Gly Leu Met  
110 115 120  
Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly  
125 130 135  
Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala  
140 145 150  
Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys  
155 160 165  
Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly  
170 175 180  
Asp Thr Val Glu Asn  
185

<210> 212  
<211> 1706  
<212> DNA  
<213> Homo sapiens

<400> 212  
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atgaaataat ttaaaagggc ttcgctcata tataggaaaa tcgcatatgg 150  
tcctagtatt aaattcttat tgcttactga tttttttgag ttaagagttg 200  
ttatatgcta gaatatgagg atgtgaatat aaataagaga agaaaaaaga 250  
ataaagtaga ttgagtctcc aattttatgt aagcttcaga agaactgggt 300  
tgtttacatg caagcttata gttgaaatat ttttcaggaa ttacatgaat 350  
gacagtcttc gaaccaatgt gtttgttcga tttcaaccag agactatagc 400  
atgtgcttgc atctaccttg cagctagagc acttcagatt ccgttgccaa 450  
ctcgtcccca ttggtttctt ctttttggtta ctacagaaga ggaaatccag 500  
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ccaaattaaa agcaaaggga ttgaatccgg atggaactcc agccctttca 650  
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aagaacctga ggatagacaa caggcttcca aaagccctta caatggtgta 800  
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gtcaagaaca cgatcacggt ctagatcaca tactccaaga agacactata 900  
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tcccgagtc acagtgaag ccctcgaaga catcataatc atggttctcc 1000  
tcaccttaag gccaaagcata ccagagatga tttaaaaagt tcaaacagac 1050  
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gatcactcag atgcagccaa gaaacacagg catgaaaggg gacatcatag 1150  
ggacaggcgt gaacgatctc gtccttttga gaggtcccat aaaagcaagc 1200  
accatggtgg cagtcgctca ggacatggca ggcacaggcg ctgactttct 1250  
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gtatggactc aatcaaaaac attaaacgca aactgattag gatttgattt 1350  
cttgaaaccc tctaggtctc tagaactctg aggacagttt cttttgaaaa 1400  
gaactatggt aatttttttg cacattaaaa tgccctagca gtatctaatt 1450  
aaaaaccatg gtcaggttca attgtacttt attatagttg tgtattgttt 1500  
attgctataa gaactggagc gtgaattctg taaaaatgta tcttattttt 1550  
atacagataa aattgcagac actgttctat ttaagtgggt atttgtttaa 1600  
atgatgggtga atactttctt aacactgggt tgtctgcatg tgtaaagatt 1650  
tttacaagga aataaaatac aaatcttggt ttttctaaaa aaaaaaaaaa 1700

aaaagt 1706

<210> 213  
<211> 299  
<212> PRT  
<213> Homo sapiens

<400> 213

Met	Asn	Asp	Ser	Leu	Arg	Thr	Asn	Val	Phe	Val	Arg	Phe	Gln	Pro	
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Glu	Thr	Ile	Ala	Cys	Ala	Cys	Ile	Tyr	Leu	Ala	Ala	Arg	Ala	Leu	
				20					25					30	
Gln	Ile	Pro	Leu	Pro	Thr	Arg	Pro	His	Trp	Phe	Leu	Leu	Phe	Gly	
				35					40					45	
Thr	Thr	Glu	Glu	Glu	Ile	Gln	Glu	Ile	Cys	Ile	Glu	Thr	Leu	Arg	
				50					55					60	
Leu	Tyr	Thr	Arg	Lys	Lys	Pro	Asn	Tyr	Glu	Leu	Leu	Glu	Lys	Glu	
				65					70					75	
Val	Glu	Lys	Arg	Lys	Val	Ala	Leu	Gln	Glu	Ala	Lys	Leu	Lys	Ala	
				80					85					90	
Lys	Gly	Leu	Asn	Pro	Asp	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Leu	Gly	
				95					100					105	
Gly	Phe	Ser	Pro	Ala	Ser	Lys	Pro	Ser	Ser	Pro	Arg	Glu	Val	Lys	
				110					115					120	
Ala	Glu	Glu	Lys	Ser	Pro	Ile	Ser	Ile	Asn	Val	Lys	Thr	Val	Lys	
				125					130					135	
Lys	Glu	Pro	Glu	Asp	Arg	Gln	Gln	Ala	Ser	Lys	Ser	Pro	Tyr	Asn	
				140					145					150	
Gly	Val	Arg	Lys	Asp	Ser	Lys	Arg	Ser	Arg	Asn	Ser	Arg	Ser	Ala	
				155					160					165	
Ser	Arg	Ser	Arg	Ser	Arg	Thr	Arg	Ser	Arg	Ser	Arg	Ser	His	Thr	
				170					175					180	
Pro	Arg	Arg	His	Tyr	Asn	Asn	Arg	Arg	Ser	Arg	Ser	Gly	Thr	Tyr	
				185					190					195	
Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	His	Ser	Glu	Ser	Pro	
				200					205					210	
Arg	Arg	His	His	Asn	His	Gly	Ser	Pro	His	Leu	Lys	Ala	Lys	His	
				215					220					225	
Thr	Arg	Asp	Asp	Leu	Lys	Ser	Ser	Asn	Arg	His	Gly	His	Lys	Arg	
				230					235					240	
Lys	Lys	Ser	Arg	Ser	Arg	Ser	Gln	Ser	Lys	Ser	Arg	Asp	His	Ser	
				245					250					255	
Asp	Ala	Ala	Lys	Lys	His	Arg	His	Glu	Arg	Gly	His	His	Arg	Asp	
				260					265					270	
Arg	Arg	Glu	Arg	Ser	Arg	Ser	Phe	Glu	Arg	Ser	His	Lys	Ser	Lys	



275

280

285

His His Gly Gly Ser Arg Ser Gly His Gly Arg His Arg Arg  
290 295

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<211> 730  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> 72-73, 85, 91, 127, 226, 268, 454, 484, 513, 566, 663  
<223> unknown base

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agccctttca accctgggtg gattttctcc 730

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<212> DNA  
<213> Homo sapiens

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ctctgtaacg gcagtttgtt ccgatacaag caccctctg aggaggagct 200  
tcggggccctg gcggggaagc cgaggccag aggcaggaaa gagcgggtggg 250  
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<210> 216

<211> 479  
 <212> PRT  
 <213> Homo sapiens

<400> 216

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Leu	Leu	Cys	Asn	Gly	Ser	Leu	Phe	Arg	Tyr	Lys	His	Pro	Ser	Glu	35	40	45	
Glu	Glu	Leu	Arg	Ala	Leu	Ala	Gly	Lys	Pro	Arg	Pro	Arg	Gly	Arg	50	55	60	
Lys	Glu	Arg	Trp	Ala	Asn	Gly	Leu	Ser	Glu	Glu	Lys	Pro	Leu	Ser	65	70	75	
Val	Pro	Arg	Asp	Ala	Pro	Phe	Gln	Leu	Glu	Thr	Cys	Pro	Leu	Thr	80	85	90	
Thr	Val	Asp	Ala	Leu	Val	Leu	Arg	Phe	Phe	Leu	Glu	Tyr	Gln	Trp	95	100	105	
Phe	Val	Asp	Phe	Ala	Val	Tyr	Ser	Gly	Gly	Val	Tyr	Leu	Phe	Thr	110	115	120	
Glu	Ala	Tyr	Tyr	Tyr	Met	Leu	Gly	Pro	Ala	Lys	Glu	Thr	Asn	Ile	125	130	135	
Ala	Val	Phe	Trp	Cys	Leu	Leu	Thr	Val	Thr	Phe	Ser	Ile	Lys	Met	140	145	150	
Phe	Leu	Thr	Val	Thr	Arg	Leu	Tyr	Phe	Ser	Ala	Glu	Glu	Gly	Gly	155	160	165	
Glu	Arg	Ser	Val	Cys	Leu	Thr	Phe	Ala	Phe	Leu	Phe	Leu	Leu	Leu	170	175	180	
Ala	Met	Leu	Val	Gln	Val	Val	Arg	Glu	Glu	Thr	Leu	Glu	Leu	Gly	185	190	195	
Leu	Glu	Pro	Gly	Leu	Ala	Ser	Met	Thr	Gln	Asn	Leu	Glu	Pro	Leu	200	205	210	
Leu	Lys	Lys	Gln	Gly	Trp	Asp	Trp	Ala	Leu	Pro	Val	Ala	Lys	Leu	215	220	225	
Ala	Ile	Arg	Val	Gly	Leu	Ala	Val	Val	Gly	Ser	Val	Leu	Gly	Ala	230	235	240	
Phe	Leu	Thr	Phe	Pro	Gly	Leu	Arg	Leu	Ala	Gln	Thr	His	Arg	Asp	245	250	255	
Ala	Leu	Thr	Met	Ser	Glu	Asp	Arg	Pro	Met	Leu	Gln	Phe	Leu	Leu	260	265	270	
His	Thr	Ser	Phe	Leu	Ser	Pro	Leu	Phe	Ile	Leu	Trp	Leu	Trp	Thr	275	280	285	
Lys	Pro	Ile	Ala	Arg	Asp	Phe	Leu	His	Gln	Pro	Pro	Phe	Gly	Glu				

290										295										300									
Thr	Arg	Phe	Ser	Leu	Leu	Ser	Asp	Ser	Ala	Phe	Asp	Ser	Gly	Arg															
				305					310					315															
Leu	Trp	Leu	Leu	Val	Val	Leu	Cys	Leu	Leu	Arg	Leu	Ala	Val	Thr															
				320					325					330															
Arg	Pro	His	Leu	Gln	Ala	Tyr	Leu	Cys	Leu	Ala	Lys	Ala	Arg	Val															
				335					340					345															
Glu	Gln	Leu	Arg	Arg	Glu	Ala	Gly	Arg	Ile	Glu	Ala	Arg	Glu	Ile															
				350					355					360															
Gln	Gln	Arg	Val	Val	Arg	Val	Tyr	Cys	Tyr	Val	Thr	Val	Val	Ser															
				365					370					375															
Leu	Gln	Tyr	Leu	Thr	Pro	Leu	Ile	Leu	Thr	Leu	Asn	Cys	Thr	Leu															
				380					385					390															
Leu	Leu	Lys	Thr	Leu	Gly	Gly	Tyr	Ser	Trp	Gly	Leu	Gly	Pro	Ala															
				395					400					405															
Pro	Leu	Leu	Ser	Pro	Asp	Pro	Ser	Ser	Ala	Ser	Ala	Ala	Pro	Ile															
				410					415					420															
Gly	Ser	Gly	Glu	Asp	Glu	Val	Gln	Gln	Thr	Ala	Ala	Arg	Ile	Ala															
				425					430					435															
Gly	Ala	Leu	Gly	Gly	Leu	Leu	Thr	Pro	Leu	Phe	Leu	Arg	Gly	Val															
				440					445					450															
Leu	Ala	Tyr	Leu	Ile	Trp	Trp	Thr	Ala	Ala	Cys	Gln	Leu	Leu	Ala															
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<210> 217  
 <211> 574  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 5, 146  
 <223> unknown base

<400> 217  
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<210> 218  
<211> 2571  
<212> DNA  
<213> Homo sapiens

<400> 218  
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ggctggtttg ggcccttgta gctgacagaa ggtggccagg gagaatgcag 200  
cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggct 250  
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aggcgctcac aagatggctg tccagacggc tgtgcgagcc tcacagccac 400  
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<211> 632

<212> PRT

<213> Homo sapiens

<400> 219

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 <211> 773  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 gtttttaaca tcatcagccc aagcaacaat ggtggcaatg ttcaggagac 200  
 agtgacaatt gataatgaaa aaaataccgc catcgttaac atccatgcag 250  
 gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300  
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<210> 221  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
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 Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu  
 35 40 45  
 Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser  
 50 55 60  
 Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val  
 65 70 75  
 Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn  
 80 85 90

Ile	Pro	Pro	Leu	Asn	Asn	Leu	Gln	Trp	Tyr	Ile	Tyr	Glu	Lys	Gln
				95					100					105
Ala	Leu	Asp	Asn	Met	Phe	Ser	Asn	Lys	Tyr	Thr	Trp	Val	Lys	Tyr
				110					115					120
Asn	Pro	Leu	Glu	Ser	Leu	Ile	Lys	Asp	Val	Asp	Trp	Phe	Leu	Leu
				125					130					135
Gly	Ser	Pro	Ile	Glu	Lys	Leu	Cys	Lys	His	Ile	Pro	Leu	Tyr	Lys
				140					145					150
Gly	Glu	Val	Val	Glu	Asn	Thr	His	Asn	Val	Gly	Ala	Gly	Gly	Cys
				155					160					165
Ala	Lys	Ala	Gly	Leu	Leu	Gly	Ile	Leu	Gly	Ile	Ser	Ile	Cys	Ala
				170					175					180

Asp Ile His Val

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 <211> 992  
 <212> DNA  
 <213> Homo sapiens

<400> 222  
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<210> 224  
 <211> 1297  
 <212> DNA  
 <213> Homo sapiens

<400> 224  
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 ctctcttttgc tatgacatca ccgtcatccc taagttcaga cctggaccac 150  
 ggtggtgtgc ggttcaaggc caggtggatg aaaagacttt tcttcactat 200  
 gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250  
 aaatgtcaca acggcctgga aagcacagaa cccagtactg agagaggtgg 300  
 tggacatact tacagagcaa ctgcgtgaca ttcagctgga gaattacaca 350  
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 tgatatttaa ataaagagtt ctatttccca aaaaaaaaaa aaaaaaa 1297

<210> 225  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens



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agcagaagac tcaacctggc ctcccataaa caggacagat tattcaggtg 350  
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attccaaaaa gaaaactcaa attgggagggc caaccacag aacagcattt 450  
ctggggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500  
cttttttccc caaaattaac acattgtgga gaagtgatga tactctcccc 550  
ttacctttcc tctctccatt caagcattca aagtatattt tcaatgaatt 600  
aaaccttgca gcaagggacc ttagatagggc ttattctgac tgtatgcttt 650  
accaatgaga gaaaaaaatg catttcctgt atcatccttt tcaataaaact 700  
gtattcattt tgaaaaaaa aaaaaaaaa aaaaa 735

<210> 227  
<211> 115  
<212> PRT  
<213> Homo sapiens

<400> 227  
Met Glu Leu Ile Pro Thr Ile Thr Ser Trp Arg Val Leu Ile Leu  
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Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly  
20 25 30  
Phe His Leu Gln Asn His Glu Leu Trp Leu Leu Ile Lys Arg Glu  
35 40 45  
Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys  
50 55 60  
Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr  
65 70 75  
Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu  
80 85 90  
Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln  
95 100 105  
Pro Thr Glu Gln His Phe Trp Ala Arg Leu  
110 115

<210> 228  
<211> 2185  
<212> DNA  
<213> Homo sapiens

<400> 228  
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cacaccatga agctcttgtg gcaggtaact gtgcaccacc acacctggaa 100

tgccatcctg ctcccgttgc totacctcac ggcgcaagtg tggattctgt 150  
 gtgcagccat cgctgctgcc gcctcagccg ggccccagaa ctgcccctcc 200  
 gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgccgggg 250  
 cctctccgag gtcccgcagg gtattccctc gaacacccgg tacctcaacc 300  
 tcatggagaa caacatccag atgatccagg ccgacacctt ccgccacctc 350  
 caccacctgg aggtcctgca gttgggcagg aactccatcc ggagattga 400  
 ggtggggggc ttcaacggcc tggccagcct caacaccctg gagctgttcg 450  
 acaactggct gacagtcac cctagcgggg cctttgaata cctgtccaag 500  
 ctgcggggagc tctggcttgc caacaacccc atcgaaagca tcccctctta 550  
 cgccttcaac cgggtgccct ccctcatgcg cctggacttg ggggagctca 600  
 agaagctgga gtatatctct gagggagctt ttgaggggct gttcaacctc 650  
 aagtatctga acttgggcat gtgcaacatt aaagacatgc ccaatctcac 700  
 ccccctggtg gggctggagg agctggagat gtcagggaac cacttccctg 750  
 agatcaggcc tggctccttc catggcctga gctccctcaa gaagctctgg 800  
 gtcatgaact cacaggtcag cctgattgag cggaatgctt ttgacgggct 850  
 ggcttcaact gtggaactca acttggccca caataacctc tcttctttgc 900  
 cccatgacct ctttaccocg ctgaggtacc tgggtggagt gcatctacac 950  
 cacaaccctt ggaactgtga ttgtgacatt ctgtggctag cctgggtggct 1000  
 tcgagagtat ataccaccca attccacctg ctgtggccgc tgtcatgctc 1050  
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 cagtgtctcg ccccttcat catggacgca cctcgagacc tcaacatttc 1150  
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 ccaaggatct ctgtcctcaa cgacggcacc ttgaactttt cccacgtgct 1300  
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 ggcccactgg acagaaaaca gcctggggaa ctctctgcac cccacagtca 1950  
 ccactatctc tgaaccttat ataattcaga cccataccaa ggacaaggta 2000  
 caggaaactc aaatatgact cccctcccc aaaaaactta taaaatgcaa 2050  
 tagaatgcac acaaagacag caacttttgt acagagtggg gagagacttt 2100  
 ttcttgata tgcttatata ttaagtctat gggctgggta aaaaaaacag 2150  
 attatattaa aatttaaaga caaaaagtca aaaca 2185

<210> 229  
 <211> 653  
 <212> PRT  
 <213> Homo sapiens

<400> 229  
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 Ala Ile Leu Leu Pro Phe Val Tyr Leu Thr Ala Gln Val Trp Ile  
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 Leu Cys Ala Ala Ile Ala Ala Ala Ala Ser Ala Gly Pro Gln Asn  
 35 40 45  
 Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val  
 50 55 60  
 Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser  
 65 70 75  
 Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile  
 80 85 90  
 Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln  
 95 100 105  
 Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn  
 110 115 120  
 Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu  
 125 130 135  
 Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg  
 140 145 150  
 Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr  
 155 160 165  
 Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu  
 170 175 180  
 Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu





	500	505	510
Thr Thr Asp Lys	Met Gln Thr Ser Leu	Asp Glu Val Met Lys	Thr
	515	520	525
Thr Lys Ile Ile	Ile Gly Cys Phe Val	Ala Val Thr Leu Leu	Ala
	530	535	540
Ala Ala Met Leu	Ile Val Phe Tyr Lys	Leu Arg Lys Arg His	Gln
	545	550	555
Gln Arg Ser Thr	Val Thr Ala Ala Arg	Thr Val Glu Ile Ile	Gln
	560	565	570
Val Asp Glu Asp	Ile Pro Ala Ala Thr	Ser Ala Ala Ala Thr	Ala
	575	580	585
Ala Pro Ser Gly	Val Ser Gly Glu Gly	Ala Val Val Leu Pro	Thr
	590	595	600
Ile His Asp His	Ile Asn Tyr Asn Thr	Tyr Lys Pro Ala His	Gly
	605	610	615
Ala His Trp Thr	Glu Asn Ser Leu Gly	Asn Ser Leu His Pro	Thr
	620	625	630
Val Thr Thr Ile	Ser Glu Pro Tyr Ile	Ile Gln Thr His Thr	Lys
	635	640	645
Asp Lys Val Gln	Glu Thr Gln Ile		
	650		

<210> 230  
 <211> 2846  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
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 tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150  
 tcgggagtg tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200  
 gggaagtctt ggggttatacc atcccttgct gcaggaatga ggagaatgag 250  
 tgtgactcct gcctgatcca cccaggttgt accatctttg aaaactgcaa 300  
 gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350  
 aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400  
 atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450  
 aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg 500  
 ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550  
 atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600  
 ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

gcataggatc ctcaactccac gtcctcttcc actccgatgg ctccaagaat 700  
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 cccttgtttc catgacggca cgtgcgctct tgacaaggct ggatcttaca 800  
 agtgtgcctg cttggcaggc tatactgggc agcgctgtga aaatctcctt 850  
 gaagaaagaa actgctcaga ccctgggggc ccagtcaatg ggtaccagaa 900  
 aataacaggg ggccctgggc ttatcaacgg acgccatgct aaaattggca 950  
 ccgtgggtgtc tttcttttgt aacaactcct atgttcttag tggcaatgag 1000  
 aaaagaactt gccagcagaa tggagagtgg tcagggaac agcccatctg 1050  
 cataaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag 1100  
 ttcttccgat gcaggttcag tcaagggaga caccattaca ccagctatac 1150  
 tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc 1200  
 agcccttccc tttggagatc tgcccatggg ataccaacat ctgcataccc 1250  
 agctccagta tgagtgcac tcaccttct accgccgcct gggcagcagc 1300  
 aggaggacat gtctgaggac tgggaagtgg agtgggcggg caccatcctg 1350  
 catccctatc tgccggaaaa ttgagaacat cactgctcca aagacccaag 1400  
 ggttgcgctg gccgtggcag gcagccatct acaggaggac cagcggggtg 1450  
 catgacggca gcctacacaa gggagcgtgg ttcctagtct gcagcgggtg 1500  
 cctggtgaat gagcgcactg tgggtggtgg tgccactgt gttactgacc 1550  
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 aaattctacc gggatgatga ccgggatgag aagaccatcc agagcctaca 1650  
 gatttctgct atcattctgc atcccaacta tgaccccatc ctgcttgatg 1700  
 ctgacatcgc catcctgaag ctctagaca aggcccgat cagcaccga 1750  
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 ctatgataaa acatgcagcc acaggctctc cactgccttc accaaggtgc 2150  
 tgccttttaa agactggatt gaaagaaata tgaaatgaac catgctcatg 2200  
 cactccttga gaagtgttcc tgtatatccg tctgtacgtg tgtcattgcg 2250



Phe	Val	Met	Leu	Ser	Leu	Glu	Phe	Asp	Tyr	Met	Cys	Gln	Tyr	Asp	
				170					175					180	
Tyr	Val	Glu	Val	Arg	Asp	Gly	Asp	Asn	Arg	Asp	Gly	Gln	Ile	Ile	
				185					190					195	
Lys	Arg	Val	Cys	Gly	Asn	Glu	Arg	Pro	Ala	Pro	Ile	Gln	Ser	Ile	
				200					205					210	
Gly	Ser	Ser	Leu	His	Val	Leu	Phe	His	Ser	Asp	Gly	Ser	Lys	Asn	
				215					220					225	
Phe	Asp	Gly	Phe	His	Ala	Ile	Tyr	Glu	Glu	Ile	Thr	Ala	Cys	Ser	
				230					235					240	
Ser	Ser	Pro	Cys	Phe	His	Asp	Gly	Thr	Cys	Val	Leu	Asp	Lys	Ala	
				245					250					255	
Gly	Ser	Tyr	Lys	Cys	Ala	Cys	Leu	Ala	Gly	Tyr	Thr	Gly	Gln	Arg	
				260					265					270	
Cys	Glu	Asn	Leu	Leu	Glu	Glu	Arg	Asn	Cys	Ser	Asp	Pro	Gly	Gly	
				275					280					285	
Pro	Val	Asn	Gly	Tyr	Gln	Lys	Ile	Thr	Gly	Gly	Pro	Gly	Leu	Ile	
				290					295					300	
Asn	Gly	Arg	His	Ala	Lys	Ile	Gly	Thr	Val	Val	Ser	Phe	Phe	Cys	
				305					310					315	
Asn	Asn	Ser	Tyr	Val	Leu	Ser	Gly	Asn	Glu	Lys	Arg	Thr	Cys	Gln	
				320					325					330	
Gln	Asn	Gly	Glu	Trp	Ser	Gly	Lys	Gln	Pro	Ile	Cys	Ile	Lys	Ala	
				335					340					345	
Cys	Arg	Glu	Pro	Lys	Ile	Ser	Asp	Leu	Val	Arg	Arg	Arg	Val	Leu	
				350					355					360	
Pro	Met	Gln	Val	Gln	Ser	Arg	Glu	Thr	Pro	Leu	His	Gln	Leu	Tyr	
				365					370					375	
Ser	Ala	Ala	Phe	Ser	Lys	Gln	Lys	Leu	Gln	Ser	Ala	Pro	Thr	Lys	
				380					385					390	
Lys	Pro	Ala	Leu	Pro	Phe	Gly	Asp	Leu	Pro	Met	Gly	Tyr	Gln	His	
				395					400					405	
Leu	His	Thr	Gln	Leu	Gln	Tyr	Glu	Cys	Ile	Ser	Pro	Phe	Tyr	Arg	
				410					415					420	
Arg	Leu	Gly	Ser	Ser	Arg	Arg	Thr	Cys	Leu	Arg	Thr	Gly	Lys	Trp	
				425					430					435	
Ser	Gly	Arg	Ala	Pro	Ser	Cys	Ile	Pro	Ile	Cys	Gly	Lys	Ile	Glu	
				440					445					450	
Asn	Ile	Thr	Ala	Pro	Lys	Thr	Gln	Gly	Leu	Arg	Trp	Pro	Trp	Gln	
				455					460					465	
Ala	Ala	Ile	Tyr	Arg	Arg	Thr	Ser	Gly	Val	His	Asp	Gly	Ser	Leu	
				470					475					480	

His	Lys	Gly	Ala	Trp 485	Phe	Leu	Val	Cys	Ser 490	Gly	Ala	Leu	Val	Asn 495
Glu	Arg	Thr	Val	Val 500	Val	Ala	Ala	His	Cys 505	Val	Thr	Asp	Leu	Gly 510
Lys	Val	Thr	Met	Ile 515	Lys	Thr	Ala	Asp	Leu 520	Lys	Val	Val	Leu	Gly 525
Lys	Phe	Tyr	Arg	Asp 530	Asp	Asp	Arg	Asp	Glu 535	Lys	Thr	Ile	Gln	Ser 540
Leu	Gln	Ile	Ser	Ala 545	Ile	Ile	Leu	His	Pro 550	Asn	Tyr	Asp	Pro	Ile 555
Leu	Leu	Asp	Ala	Asp 560	Ile	Ala	Ile	Leu	Lys 565	Leu	Leu	Asp	Lys	Ala 570
Arg	Ile	Ser	Thr	Arg 575	Val	Gln	Pro	Ile	Cys 580	Leu	Ala	Ala	Ser	Arg 585
Asp	Leu	Ser	Thr	Ser 590	Phe	Gln	Glu	Ser	His 595	Ile	Thr	Val	Ala	Gly 600
Trp	Asn	Val	Leu	Ala 605	Asp	Val	Arg	Ser	Pro 610	Gly	Phe	Lys	Asn	Asp 615
Thr	Leu	Arg	Ser	Gly 620	Val	Val	Ser	Val	Val 625	Asp	Ser	Leu	Leu	Cys 630
Glu	Glu	Gln	His	Glu 635	Asp	His	Gly	Ile	Pro 640	Val	Ser	Val	Thr	Asp 645
Asn	Met	Phe	Cys	Ala 650	Ser	Trp	Glu	Pro	Thr 655	Ala	Pro	Ser	Asp	Ile 660
Cys	Thr	Ala	Glu	Thr 665	Gly	Gly	Ile	Ala	Ala 670	Val	Ser	Phe	Pro	Gly 675
Arg	Ala	Ser	Pro	Glu 680	Pro	Arg	Trp	His	Leu 685	Met	Gly	Leu	Val	Ser 690
Trp	Ser	Tyr	Asp	Lys 695	Thr	Cys	Ser	His	Arg 700	Leu	Ser	Thr	Ala	Phe 705
Thr	Lys	Val	Leu	Pro 710	Phe	Lys	Asp	Trp	Ile 715	Glu	Arg	Asn	Met	Lys 720

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic oligonucleotide probe

<400> 232

aggttcgtga tggagacaac cgcg 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence



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 aacacaatcc tttatatatc aacatcacag tggatttctg gtttggtgca 1150  
 tgaccctgga tcttttgggtg atgtttggaa gaactgattc tttgtttgca 1200  
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 acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag 1300  
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 gtgaaaaagc aaaa 1964

<210> 236  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> Signal peptide  
 <222> 1-27  
 <223> Signal peptide

<220>  
 <221> N-glycosylation sites  
 <222> 4-7, 220-223, 335-338  
 <223> N-glycosylation sites

<220>  
 <221> Xylose isomerase proteins  
 <222> 191-201  
 <223> Xylose isomerase proteins

<400> 236  
 Met Gly Phe Asn Leu Thr Phe His Leu Ser Tyr Lys Phe Arg Leu  
 1 5 10 15





Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala  
 335 340

<210> 237  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 ccttacctca gaggccagag caagc 25

<210> 238  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 238  
 gagcttcacgc cgttctgcgt tcacc 25

<210> 239  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 239  
 caggaatgta aagctttaca gagggtcgcc atcctcgttc cccacc 46

<210> 240  
 <211> 2567  
 <212> DNA  
 <213> Homo sapiens

<400> 240  
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 tctcccgcctc cgggccccgc aatggcccag gcagtgtggt cgcgcctcgc 150  
 ccgcacccctc tggcttgccct gcctcctgcc ctgggccccgc gcaggggtgg 200  
 ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250  
 ggagcgggtg tgaccatctc ggccagcctg gtggccaagg acaacggcag 300  
 cctggccctg cccgctgacg cccacctota ccgcttcac tgcatccaca 350  
 ccccgcctgg gcttactggc aagatggaga agggctctcag ctccaccatc 400  
 cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tctgggtcac 450  
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 tccccatcac agagttcctc gtgggggacc ttgttgcac ccagaacact 550



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 aggccttgca gcggtagaag aggttgagtc aaggccgggc gcggtggctc 2300  
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 aaaaaaatac aaaaagttag ccgggcgtgg tgggtgggtgc ctgtagtccc 2450  
 agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500  
 gcttgcaagt agcccagatg gcgccactgc actccagcct gagtgcacaga 2550  
 gcgagactct gtctcca 2567

<210> 241  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 241  
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 Tyr Glu Leu Asn Leu Thr Thr Asp Ser Pro Ala Thr Thr Gly Ala  
 35 40 45  
 Val Val Thr Ile Ser Ala Ser Leu Val Ala Lys Asp Asn Gly Ser  
 50 55 60  
 Leu Ala Leu Pro Ala Asp Ala His Leu Tyr Arg Phe His Trp Ile  
 65 70 75  
 His Thr Pro Leu Val Leu Thr Gly Lys Met Glu Lys Gly Leu Ser  
 80 85 90  
 Ser Thr Ile Arg Val Val Gly His Val Pro Gly Glu Phe Pro Val  
 95 100 105  
 Ser Val Trp Val Thr Ala Ala Asp Cys Trp Met Cys Gln Pro Val  
 110 115 120  
 Ala Arg Gly Phe Val Val Leu Pro Ile Thr Glu Phe Leu Val Gly  
 125 130 135  
 Asp Leu Val Val Thr Gln Asn Thr Ser Leu Pro Trp Pro Ser Ser  
 140 145 150  
 Tyr Leu Thr Lys Thr Val Leu Lys Val Ser Phe Leu Leu His Asp  
 155 160 165  
 Pro Ser Asn Phe Leu Lys Thr Ala Leu Phe Leu Tyr Ser Trp Asp  
 170 175 180  
 Phe Gly Asp Gly Thr Gln Met Val Thr Glu Asp Ser Val Val Tyr  
 185 190 195

Tyr	Asn	Tyr	Ser	Ile	Ile	Gly	Thr	Phe	Thr	Val	Lys	Leu	Lys	Val
				200					205					210
Val	Ala	Glu	Trp	Glu	Glu	Val	Glu	Pro	Asp	Ala	Thr	Arg	Ala	Val
				215					220					225
Lys	Gln	Lys	Thr	Gly	Asp	Phe	Ser	Ala	Ser	Leu	Lys	Leu	Gln	Glu
				230					235					240
Thr	Leu	Arg	Gly	Ile	Gln	Val	Leu	Gly	Pro	Thr	Leu	Ile	Gln	Thr
				245					250					255
Phe	Gln	Lys	Met	Thr	Val	Thr	Leu	Asn	Phe	Leu	Gly	Ser	Pro	Pro
				260					265					270
Leu	Thr	Val	Cys	Trp	Arg	Leu	Lys	Pro	Glu	Cys	Leu	Pro	Leu	Glu
				275					280					285
Glu	Gly	Glu	Cys	His	Pro	Val	Ser	Val	Ala	Ser	Thr	Ala	Tyr	Asn
				290					295					300
Leu	Thr	His	Thr	Phe	Arg	Asp	Pro	Gly	Asp	Tyr	Cys	Phe	Ser	Ile
				305					310					315
Arg	Ala	Glu	Asn	Ile	Ile	Ser	Lys	Thr	His	Gln	Tyr	His	Lys	Ile
				320					325					330
Gln	Val	Trp	Pro	Ser	Arg	Ile	Gln	Pro	Ala	Val	Phe	Ala	Phe	Pro
				335					340					345
Cys	Ala	Thr	Leu	Ile	Thr	Val	Met	Leu	Ala	Phe	Ile	Met	Tyr	Met
				350					355					360
Thr	Leu	Arg	Asn	Ala	Thr	Gln	Gln	Lys	Asp	Met	Val	Glu	Asn	Pro
				365					370					375
Glu	Pro	Pro	Ser	Gly	Val	Arg	Cys	Cys	Cys	Gln	Met	Cys	Cys	Gly
				380					385					390
Pro	Phe	Leu	Leu	Glu	Thr	Pro	Ser	Glu	Tyr	Leu	Glu	Ile	Val	Arg
				395					400					405
Glu	Asn	His	Gly	Leu	Leu	Pro	Pro	Leu	Tyr	Lys	Ser	Val	Lys	Thr
				410					415					420

Tyr Thr Val

<210> 242  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 242  
 catttcctta ccctggaccc agctcc 26

<210> 243  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
gaaaggccca cagcacatct ggcag 25

<210> 244  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 244  
ccacgacccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245  
<211> 485  
<212> DNA  
<213> Homo sapiens

<400> 245  
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50  
gctcccagat ctgggcccgt tgctctctgc tctctctcct cctcgccagc 100  
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150  
gcaacccag gacagagctg gagccagggc cagctggatg cccatgttcc 200  
agaggcgaag gaggcgagac acccacttcc ccactctgcat tttctgctgc 250  
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300  
acctgccctg ccccgctccc ctcccttctt tattttattcc tgctgcccc 350  
gaacataggt cttggaataa aatggctggg tcttttgttt tccaaaaaaaa 400  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> 246  
<211> 84  
<212> PRT  
<213> Homo sapiens

<400> 246  
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln  
20 25 30  
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala  
35 40 45  
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp  
50 55 60  
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg  
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr

80

<210> 247  
<211> 2359  
<212> DNA  
<213> Homo sapiens

<400> 247  
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agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcaccct 150  
ccttctcggt ttcacatag tgccagccat ttttgagtc tcctttggtg 200  
tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250  
ttgagaatgg agcaggaggc caaggagaag aaccaccagc tttacaagcc 300  
ctacaccaac ggaatcattg caaaggatcc cacttcacta gaagaagaga 350  
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gagttcgagc tctctgacat tttctacttt tgccggaaag gaatggagac 450  
cattatggat gatgagggtga caaagagatt ctgagcagaa gaactggagt 500  
cctggaacct gctgagcaga accaattata acttcagta catcagcctt 550  
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gctgccgctc aggatagcac tggttttcac agggattagc cttctggtgg 650  
tgggcacaac tgtggtggga tacttgccaa atgggaggtt taaggaattc 700  
atgagtaaac atgttcaatt aatgtgttac cggatctgcg tgcgagcgt 750  
gacagccatc atcacctacc atgacaggga aaacagacca agaaatggtg 800  
gcatctgtgt ggccaatcat acctcaccga togatgtgat catcttggcc 850  
agcgatggct attatgccat ggtgggtcaa gtgcacgggg gactcatggg 900  
tgtgattcag agagccatgg tgaaggcctg cccacacgtc tggtttgagc 950  
gctcggaagt gaaggatcgc cacctggtgg ctaagagact gactgaacat 1000  
gtgcaagata aaagcaagct gcctatcctc atcttcccag aaggaacctg 1050  
catcaataat acatcgggtg tgatgttcaa aaaggaagt tttgaaattg 1100  
gagccacagt ttacctgtt gctatcaagt atgacctca atttggcgat 1150  
gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200  
gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250  
ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300  
gccattgcca ggcaggaggg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400  
acagcaagat gatcgtgggg aaccacaagg acaggagccg ctcttgagcc 1450  
tgcctccagc tgggtggggc caccgtgcgg ggtgccaacg ggctcagagc 1500  
tggagttgcc gccgccgccc ccaactgctgt gtcctttcca gactccaggg 1550  
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cgggatccct gtgcacccgg cgcagcctac ccttggtggt ctaaaccgat 1650  
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cggccacccg ctctccagga aaggcacagc tgaggcactg tggctggctt 1900  
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gttggtgggga ttaaagtgtc gcgggtgagt gaaggacaca tcacgttcag 2250  
tgtttcaagt acaggccac aaaacggggc acggcaggcc tgagctcaga 2300  
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ggtgaatga 2359

<210> 248

<211> 456

<212> PRT

<213> Homo sapiens

<400> 248

Met	Phe	Leu	Leu	Leu	Pro	Phe	Asp	Ser	Leu	Ile	Val	Asn	Leu	Leu
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Gly	Ile	Ser	Leu	Thr	Val	Leu	Phe	Thr	Leu	Leu	Leu	Val	Phe	Ile
				20					25					30
Ile	Val	Pro	Ala	Ile	Phe	Gly	Val	Ser	Phe	Gly	Ile	Arg	Lys	Leu
				35					40					45
Tyr	Met	Lys	Ser	Leu	Leu	Lys	Ile	Phe	Ala	Trp	Ala	Thr	Leu	Arg
				50					55					60
Met	Glu	Arg	Gly	Ala	Lys	Glu	Lys	Asn	His	Gln	Leu	Tyr	Lys	Pro
				65					70					75







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gga 1103

<210> 250

<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

Met Ala Leu Ala Ala Leu Met Ile Ala Leu Gly Ser Leu Gly Leu  
1 5 10 15

His Thr Trp Gln Ala Gln Ala Val Pro Thr Ile Leu Pro Leu Gly  
20 25 30

Leu Ala Pro Asp Thr Phe Asp Asp Thr Tyr Val Gly Cys Ala Glu  
35 40 45

Glu Met Glu Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala  
50 55 60

His His Ala Leu Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr  
65 70 75

Trp Glu Asp Lys Arg Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys  
80 85 90

Ala Gln Asn Gly Ile Ala Ile Met Val Tyr Thr Asn Ser Ser Asn  
95 100 105

Thr Leu Tyr Trp Glu Leu Asn Gln Ala Val Arg Thr Gly Gly Gly  
110 115 120

Ser Arg Glu Leu Tyr Met Arg His Phe Pro Phe Lys Ala Leu His  
125 130 135

Phe Tyr Leu Ile Arg Ala Leu Gln Leu Leu Arg Gly Ser Gly Gly  
140 145 150

Cys Ser Arg Gly Pro Gly Glu Val Val Phe Arg Gly Val Gly Ser  
155 160 165

Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser Val Arg Leu Gly  
170 175 180

Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala His Arg Phe  
185 190 195

Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Val Gln Leu  
200 205 210

Gly Ser Gln Ser Glu Gly Ala Ser Ser Leu Pro Pro Trp Lys Thr  
215 220 225

Leu Leu Leu Ala Pro Gly Glu Phe Gln Leu Ser Gly Val Gly Pro  
230 235 240

<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
ccaccacctg gaggtcctgc agttgggcag gaactccatc cggcagattg 50

<210> 252  
<211> 1076  
<212> DNA  
<213> Homo sapiens

<400> 252  
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caacatgcct caccctcatc tatatccttt ggagctcac agggtcagca 100  
gcctctggac cagtgaaga gctggctcgt tccgttggtg gggccgtgac 150  
tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct 200  
tcaacacaac cctcttgtc accatacagc cagaaggggg cactatcata 250  
gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta 300  
ctccctgaag ctacgcaaac tgaagaagaa tgactcaggg atctactatg 350  
tggggatata cagctcatca ctccagcagc cctccacca ggagtacgtg 400  
ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca 450  
gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattggaac 500  
atggggaaga ggatgtgatt tatacctgga aggcctggg gcaagcagcc 550  
aatgagtccc ataatgggtc catcctcccc atctcctgga gatggggaga 600  
aagtgatatg accttcatct gcgttgccag gaaccctgtc agcagaaaact 650  
tctcaagccc catccttgcc aggaagctct gtgaagggtc tgctgatgac 700  
ccagattcct ccattggtcct cctgtgtctc ctgttggtgc cctcctgct 750  
cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac 800  
aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact 850  
cctaacatat gccccattc tggagagaac acagagtacg acacaatccc 900  
tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950  
ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg 1000  
atgccagaca caccaaggct atttgctat gagaatgtta tctagacagc 1050  
agtgcactcc cctaagtctc tgctca 1076

<210> 253  
<211> 335  
<212> PRT  
<213> Homo sapiens

<400> 253  
Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp

09989738-112004

1	5	10	15
Gln Leu Thr Gly Ser	Ala Ala Ser Gly	Pro Val Lys Glu Leu Val	20 25 30
Gly Ser Val Gly Gly	Ala Val Thr Phe	Pro Leu Lys Ser Lys Val	35 40 45
Lys Gln Val Asp Ser	Ile Val Trp Thr	Phe Asn Thr Thr Pro Leu	50 55 60
Val Thr Ile Gln Pro	Glu Gly Gly Thr	Ile Ile Val Thr Gln Asn	65 70 75
Arg Asn Arg Glu Arg	Val Asp Phe Pro	Asp Gly Gly Tyr Ser Leu	80 85 90
Lys Leu Ser Lys Leu	Lys Lys Asn Asp	Ser Gly Ile Tyr Tyr Val	95 100 105
Gly Ile Tyr Ser Ser	Ser Leu Gln Gln	Pro Ser Thr Gln Glu Tyr	110 115 120
Val Leu His Val Tyr	Glu His Leu Ser	Lys Pro Lys Val Thr Met	125 130 135
Gly Leu Gln Ser Asn	Lys Asn Gly Thr	Cys Val Thr Asn Leu Thr	140 145 150
Cys Cys Met Glu His	Gly Glu Glu Asp	Val Ile Tyr Thr Trp Lys	155 160 165
Ala Leu Gly Gln Ala	Ala Asn Glu Ser	His Asn Gly Ser Ile Leu	170 175 180
Pro Ile Ser Trp Arg	Trp Gly Glu Ser	Asp Met Thr Phe Ile Cys	185 190 195
Val Ala Arg Asn Pro	Val Ser Arg Asn	Phe Ser Ser Pro Ile Leu	200 205 210
Ala Arg Lys Leu Cys	Glu Gly Ala Ala	Asp Asp Pro Asp Ser Ser	215 220 225
Met Val Leu Leu Cys	Leu Leu Leu Val	Pro Leu Leu Leu Ser Leu	230 235 240
Phe Val Leu Gly Leu	Phe Leu Trp Phe	Leu Lys Arg Glu Arg Gln	245 250 255
Glu Glu Tyr Ile Glu	Glu Lys Lys Arg	Val Asp Ile Cys Arg Glu	260 265 270
Thr Pro Asn Ile Cys	Pro His Ser Gly	Glu Asn Thr Glu Tyr Asp	275 280 285
Thr Ile Pro His Thr	Asn Arg Thr Ile	Leu Lys Glu Asp Pro Ala	290 295 300
Asn Thr Val Tyr Ser	Thr Val Glu Ile	Pro Lys Lys Met Glu Asn	305 310 315
Pro His Ser Leu Leu	Thr Met Pro Asp	Thr Pro Arg Leu Phe Ala	

320

325

330

Tyr Glu Asn Val Ile  
335

<210> 254  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<400> 254  
ctggttcccc aacatgcctc accctcatct atatcctttg gcagctcaca 50  
gggtcagcag cctctggacc cgtgaaagag ctggtcgggt ccgttggttg 100  
ggcogtgact ttccccctga agtccaaagt aaagcaagtt gactctattg 150  
tctggacctt caacacaacc cctcttgta ccatcacagcc agaagggggc 200  
actatcatag tgacccaaaa tcgtaatagg gagagagtag acttcccaga 250  
tggaggctac tccctgaagc tcagcaaact gaagaagaat gactcagggg 300  
tctactatgt ggggatatac agctcatcac tccagcagcc ctccaccag 350  
gagtacgtgc tgcatgtcta cgagcacctg tcaaagccta aagtcacat 400  
gggtctgcag agcaataaga atggcacctg tgtgaccaat ctgacatgct 450  
gcatggaaca tggggaagag gatgtgattt atacctggaa ggccctgggg 500  
caagcagcca atgagtccca taatgggtcc atcctcccca tctcctggag 550  
atggggagaa agtgatatga ccttcatctg cgttgccagg aaccctgtca 600  
gcagaaactt ctcaagcccc atccttgcca ggaagctctg tgaagggtgct 650  
gctgatgacc cagattcctc catggtcctc ctgtgtctcc tgttggtgcc 700  
cctcctgctc agtctctttg tactgggggt atttcttttg tttctgaaga 750  
gagagagaca agaagagtag attgaagaga agaagagagt ggacatttgt 800  
cgggaaactc ctaacatatg cccccattct ggagagaaca cagagtacga 850  
cacaatccct cacactaata gaacaatcct aaaggaagat ccagcaaata 900  
cggtttactc cactgtggaa ataccgaaaa agatggaaaa tccccactca 950  
ctgctcacga tgccagacac accaaggcta tttgcctatg agaatgttat 1000  
ctagacagca gtgcaactccc ctaagtctct gctcaaaaaa aaaaaaaaaa 1050  
aaa 1053

<210> 255  
<211> 860  
<212> DNA  
<213> Homo sapiens

<400> 255  
gaaagacgtg gtcctgacag acagacaatc ctattcccta ccaaatgaa 50

gatgctgctg ctgctgtgtt tgggactgac cctagtctgt gtccatgcag 100  
aagaagctag ttctacggga aggaacttta atgtagaaaa gattaatggg 150  
gaatggcata ctattatcct ggcctctgac aaaagagaaa agatagaaga 200  
acatggcaac tttagacttt ttctggagca aatccatgtc ttggagaatt 250  
ccttagttct taaagtccat actgtaagag atgaagagtg ctccgaatta 300  
tctatggttg ctgacaaaac agaaaaggct ggtgaatatt ctgtgacgta 350  
tgatggattc aatacattta ctatacctaa gacagactat gataactttc 400  
ttatggctca cctcattaac gaaaaggatg gggaaacctt ccagctgatg 450  
gggctctatg gccgagaacc agatttgagt tcagacatca aggaaagggt 500  
tgcacaacta tgtgaggagc atggaatcct tagagaaaat atcattgacc 550  
tatccaatgc caatcgctgc ctccaggccc gagaatgaag aatggcctga 600  
gcctccagtg ttgagtggac acttctcacc aggactccac catcatccct 650  
tcctatccat acagcatccc cagtataaat tctgtgatct gcattccatc 700  
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acctcatcaa gaatcaaaga cttctttaaa tttctctttg atacaccctt 800  
gacaattttt catgaaatta ttctcttccc tgttcaataa atgattaccc 850  
ttgcacttaa 860

<210> 256

<211> 180

<212> PRT

<213> Homo sapiens

<400> 256

Met	Lys	Met	Leu	Leu	Leu	Leu	Cys	Leu	Gly	Leu	Thr	Leu	Val	Cys	
1				5					10					15	
Val	His	Ala	Glu	Glu	Ala	Ser	Ser	Thr	Gly	Arg	Asn	Phe	Asn	Val	
				20					25					30	
Glu	Lys	Ile	Asn	Gly	Glu	Trp	His	Thr	Ile	Ile	Leu	Ala	Ser	Asp	
				35					40					45	
Lys	Arg	Glu	Lys	Ile	Glu	Glu	His	Gly	Asn	Phe	Arg	Leu	Phe	Leu	
				50					55					60	
Glu	Gln	Ile	His	Val	Leu	Glu	Asn	Ser	Leu	Val	Leu	Lys	Val	His	
				65					70					75	
Thr	Val	Arg	Asp	Glu	Glu	Cys	Ser	Glu	Leu	Ser	Met	Val	Ala	Asp	
				80					85					90	
Lys	Thr	Glu	Lys	Ala	Gly	Glu	Tyr	Ser	Val	Thr	Tyr	Asp	Gly	Phe	
				95					100					105	
Asn	Thr	Phe	Thr	Ile	Pro	Lys	Thr	Asp	Tyr	Asp	Asn	Phe	Leu	Met	
				110					115					120	

Ala	His	Leu	Ile	Asn	Glu	Lys	Asp	Gly	Glu	Thr	Phe	Gln	Leu	Met
				125					130					135
Gly	Leu	Tyr	Gly	Arg	Glu	Pro	Asp	Leu	Ser	Ser	Asp	Ile	Lys	Glu
				140					145					150
Arg	Phe	Ala	Gln	Leu	Cys	Glu	Glu	His	Gly	Ile	Leu	Arg	Glu	Asn
				155					160					165
Ile	Ile	Asp	Leu	Ser	Asn	Ala	Asn	Arg	Cys	Leu	Gln	Ala	Arg	Glu
				170					175					180

<210> 257  
 <211> 766  
 <212> DNA  
 <213> Homo sapiens

<400> 257  
 ggctcgagcg tttctgagcc aggggtgacc atgacctgct gcgaaggatg 50  
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 ttotcaatgc gatacctcta attgtcagct tagttgagga agaccaat 150  
 tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg 200  
 agcaggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250  
 aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc 300  
 agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca 350  
 ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400  
 ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450  
 ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactgggtt 500  
 caataaacc accagtaacg acaccatggc gagtggctgg agagcatcta 550  
 gtttccactt cgattctgaa gaaaacaaac ataggcttat ccacttctca 600  
 gtatttttag gtctattgct tggttgaatt ctggaggtcc tgtttgggct 650  
 cagtcagata gtcacgggtt tccttggtg tctgtgtgga gtctctaagc 700  
 gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta 750  
 gtttgaaaaa aaaaaa 766

<210> 258  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 258  
 Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu  
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 Leu Val Leu Leu Leu Leu Gly Val Val Leu Asn Ala Ile Pro Leu  
 20 25 30  
 Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile



35										40					45				
Ser	Cys	Phe	Glu	Trp	Trp	Phe	Pro	Gly	Ile	Ile	Gly	Ala	Gly	Leu					
				50					55					60					
Met	Ala	Ile	Pro	Ala	Thr	Thr	Met	Ser	Leu	Thr	Ala	Arg	Lys	Arg					
				65					70					75					
Ala	Cys	Cys	Asn	Asn	Arg	Thr	Gly	Met	Phe	Leu	Ser	Ser	Phe	Phe					
				80					85					90					
Ser	Val	Ile	Thr	Val	Ile	Gly	Ala	Leu	Tyr	Cys	Met	Leu	Ile	Ser					
				95					100					105					
Ile	Gln	Ala	Leu	Leu	Lys	Gly	Pro	Leu	Met	Cys	Asn	Ser	Pro	Ser					
				110					115					120					
Asn	Ser	Asn	Ala	Asn	Cys	Glu	Phe	Ser	Leu	Lys	Asn	Ile	Ser	Asp					
				125					130					135					
Ile	His	Pro	Glu	Ser	Phe	Asn	Leu	Gln	Trp	Phe	Phe	Asn	Asp	Ser					
				140					145					150					
Cys	Ala	Pro	Pro	Thr	Gly	Phe	Asn	Lys	Pro	Thr	Ser	Asn	Asp	Thr					
				155					160					165					
Met	Ala	Ser	Gly	Trp	Arg	Ala	Ser	Ser	Phe	His	Phe	Asp	Ser	Glu					
				170					175					180					
Glu	Asn	Lys	His	Arg	Leu	Ile	His	Phe	Ser	Val	Phe	Leu	Gly	Leu					
				185					190					195					
Leu	Leu	Val	Gly	Ile	Leu	Glu	Val	Leu	Phe	Gly	Leu	Ser	Gln	Ile					
				200					205					210					
Val	Ile	Gly	Phe	Leu	Gly	Cys	Leu	Cys	Gly	Val	Ser	Lys	Arg	Arg					
				215					220					225					

Ser Gln Ile Val

<210> 259  
 <211> 434  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 gtcgaatcca aatcactcat tgtgaaagct gagctcacag ccgaataagc 50  
 caccatgagg ctgtcagtgt gtctcctgat ggtctcgctg gccctttgct 100  
 gctaccaggc ccattgctctt gtctgcccag ctgttgcttc tgagatcaca 150  
 gtcttcttat tcttaagtga cgctgcggtta aacctccaag ttgccaaact 200  
 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250  
 ccgatcagat atctttttaag aaacgactct cattgaaaaa gtcttggtgg 300  
 aaatagtga aaaatgtggt gtgtgacatg taaaaatgct caacctggtt 350  
 tccaaagtct ttcaacgaca ccctgatctt cactaaaaat tgtaaagggt 400

tcaacacggtt gctttaataa atcacttgcc ctgc 434

<210> 260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 260

Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys  
1 5 10 15

Cys Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu  
20 25 30

Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln  
35 40 45

Val Ala Lys Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu  
50 55 60

Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu  
65 70 75

Ser Leu Lys Lys Ser Trp Trp Lys  
80

<210> 261

<211> 636

<212> DNA

<213> Homo sapiens

<400> 261

atccgtttctc tgcgctgccca gctcaggtga gccctcgcca aggtgacctc 50

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ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150

cgccccagtg cctctcccc tgcagccctg cccctcgaac tgtgacatgg 200

agagagtgac cctggccctt ctctactgg caggcctgac tgcccttgaa 250

gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300

aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg 350

ggatcgcggc agttctgagt ggcaaagca aatacaagag cagccagaag 400

cagcacagtc ctgtacctga gaaggccatc ccactcatca ctccaggctc 450

tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500

taacactggc cccagcacc tcctcccctg ggaggcctta tcctcaagga 550

aggacttctc tccaagggca ggctgttagg cccctttctg atcaggaggc 600

ttctttatga attaaactcg cccaccacc ccctca 636

<210> 262

<211> 89

<212> PRT

<213> Homo sapiens

<400> 262

Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr  
1 5 10 15

Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe  
20 25 30

Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly  
35 40 45

Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys  
50 55 60

Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu  
65 70 75

Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys  
80 85

<210> 263

<211> 1676

<212> DNA

<213> Homo sapiens

<400> 263

ggagaagagg ttgtgtggga caagctgctc cgcacagaag gatgtcgctg 50  
ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct 100  
actcctgctg ctggttgtgg gctcctggct actcgccgcg atcctggctt 150  
ggacctatgc cttctataac aactgcgcgc ggctccagtg tttcccacag 200  
ccccaaaac ggaactggtt ttggggtcac ctgggcctga tctctctac 250  
agaggagggc ttgaaggact cgaccagat gtcggccacc tattcccagg 300  
gctttacggt atggctgggt cccatcatcc ccttcacgtt tttatgccac 350  
cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcaccaa 400  
ggataatctc ttcatcaggt tctgaagcc ctggctggga gaagggatac 450  
tgctgagtgg cggtgacaag tggagccgc accgtcggat gctgacgcc 500  
gccttccatt tcaacatcct gaagtctat ataacgatct tcaacaagag 550  
tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca 600  
gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta 650  
cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga 700  
atatattgcc accatcttgg agctcagtg ccttgtagag aaaagaagcc 750  
agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg 800  
cggcgcttcc acagggcctg ccgcctgggt catgaactca cagacgctgt 850  
catccgggag cggcgtcgca cctcccccac tcagggtatt gatgattttt 900  
tcaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg 950

ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc 1000  
 agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc 1050  
 tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc 1100  
 tgccgacagg aggtgcaaga gcttctgaag gaccgcatc ctaaagagat 1150  
 tgaatgggac gacctggccc agctgccctt cctgaccatg tgcgtgaagg 1200  
 agagcctgag gttacatccc ccagctccct tcctctcccg atgctgcacc 1250  
 caggacattg ttctcccaga tggccgagtc atccccaaag gcattacctg 1300  
 cctcatcgat attatagggg tccatcacia cccaactgtg tggccggatc 1350  
 ctgaggtcta cgaccccttc cgctttgacc cagagaacag caaggggagg 1400  
 tcacctctgg cttttattcc tttctccgca gggcccagga actgcatcgg 1450  
 gcaggcgttc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc 1500  
 tgcaacttccg gttcctgcca gaccacactg agccccgcag gaagctggaa 1550  
 ttgatcatgc gcgccgaggg cgggctttgg ctgcgggtgg agccctgaa 1600  
 tgtaggcttg cagtgacttt ctgaccatc cacctgtttt tttgcagatt 1650  
 gtcataaata aaacggtgct gtcaaa 1676

<210> 264  
 <211> 524  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala  
 1 5 10 15  
 Met Ser Pro Trp Leu Leu Leu Leu Leu Val Val Gly Ser Trp Leu  
 20 25 30  
 Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys  
 35 40 45  
 Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe  
 50 55 60  
 Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys  
 65 70 75  
 Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val  
 80 85 90  
 Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp  
 95 100 105  
 Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys  
 110 115 120  
 Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly  
 125 130 135



Lys	Gly	Arg	Ser	Pro	Leu	Ala	Phe	Ile	Pro	Phe	Ser	Ala	Gly	Pro
				455					460					465
Arg	Asn	Cys	Ile	Gly	Gln	Ala	Phe	Ala	Met	Ala	Glu	Met	Lys	Val
				470					475					480
Val	Leu	Ala	Leu	Met	Leu	Leu	His	Phe	Arg	Phe	Leu	Pro	Asp	His
				485					490					495
Thr	Glu	Pro	Arg	Arg	Lys	Leu	Glu	Leu	Ile	Met	Arg	Ala	Glu	Gly
				500					505					510
Gly	Leu	Trp	Leu	Arg	Val	Glu	Pro	Leu	Asn	Val	Gly	Leu	Gln	
				515					520					

<210> 265  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50  
 ctggcctcct gctgttttgc tttcacagga ttcttaaata ctctcttata 100  
 tcttcctctc cttgactcca gggaaatata ctttcaactc tcagcacctc 150  
 atgaagacgc gcgcttaact ccggaggagc tagaaagagc ttcccttcta 200  
 cagatattgc cagagatgct ggggtgcagaa agaggggata ttctcaggaa 250  
 agcagactca agtaccaaca tttttaaccc aagaggaaat ttgagaaagt 300  
 ttcaggattt ctctggacaa gatcctaaca ttttactgag tcattctttg 350  
 gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400  
 gaaataactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450  
 acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500  
 tggagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550  
 aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 266  
 Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu  
 1 5 10 15  
 Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser  
 20 25 30  
 Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu  
 35 40 45  
 Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu  
 50 55 60

Gly	Ala	Glu	Arg	Gly	Asp	Ile	Leu	Arg	Lys	Ala	Asp	Ser	Ser	Thr
				65					70					75
Asn	Ile	Phe	Asn	Pro	Arg	Gly	Asn	Leu	Arg	Lys	Phe	Gln	Asp	Phe
				80					85					90
Ser	Gly	Gln	Asp	Pro	Asn	Ile	Leu	Leu	Ser	His	Leu	Leu	Ala	Arg
				95					100					105
Ile	Trp	Lys	Pro	Tyr	Lys	Lys	Arg	Glu	Thr	Pro	Asp	Cys	Phe	Trp
				110					115					120

Lys Tyr Cys Val

<210> 267  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<400> 267  
 gaacattttt agttcccaag gaatgtacat cagccccacg gaagctaggc 50  
 cacctctggg atgggggttg tggtttaaaa caaacgccag tcatcctata 100  
 taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150  
 acctgtctgc aaccagctg aggccatgcc ctcccaggg accgtctgca 200  
 gcctcctgct cctcggcatg ctctggctgg acttggccat ggcaggctcc 250  
 agcttcctga gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300  
 gaagccacca gccaagctgc agccccgagc tctagcaggc tggctccgcc 350  
 cggaagatgg aggtcaagca gaaggggcag aggatgaact ggaagtccgg 400  
 ttcaacgccc cttttgatgt tggaatcaag ctgtcagggg ttcagtacca 450  
 gcagcacagc caggccctgg ggaagtttct tcaggacatc ctctgggaag 500  
 aggccaaaga ggccccagcc gacaagtgat cgccacaag cttactcac 550  
 ctctctctaa gtttagaagc gctcatctgg cttttcgctt gcttctgcag 600  
 caactcccac gactgttgta caagctcagg aggccaataa atgttcaaac 650  
 tgta 654

<210> 268  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 268  
 Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Gly Met  
 1 5 10 15  
 Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro  
 20 25 30  
 Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro  
 35 40 45

Ala	Lys	Leu	Gln	Pro	Arg	Ala	Leu	Ala	Gly	Trp	Leu	Arg	Pro	Glu
				50					55					60
Asp	Gly	Gly	Gln	Ala	Glu	Gly	Ala	Glu	Asp	Glu	Leu	Glu	Val	Arg
				65					70					75
Phe	Asn	Ala	Pro	Phe	Asp	Val	Gly	Ile	Lys	Leu	Ser	Gly	Val	Gln
				80					85					90
Tyr	Gln	Gln	His	Ser	Gln	Ala	Leu	Gly	Lys	Phe	Leu	Gln	Asp	Ile
				95					100					105
Leu	Trp	Glu	Glu	Ala	Lys	Glu	Ala	Pro	Ala	Asp	Lys			
				110					115					

<210> 269  
 <211> 1332  
 <212> DNA  
 <213> Homo sapiens

<400> 269  
 cggccacagc tggcatgctc tgcctgatcg ccatcctgct gtatgtcctc 50  
 gtccagtacc tcgtgaaccc cggggtgctc cgcacggacc ccagatgtca 100  
 agaatatgaa cacgtggctg ctgttctctc cctgttccc ggtgcagggtg 150  
 cagaccctga tagtcgtgat catcgggatg ctctgtctcc tgctggactt 200  
 tcttggttg gtgcacctgg gccagctgct catcttccac atctacctga 250  
 gtatgtcccc caccctaagc ccccgatccc cccaaggctg ggtggtcaga 300  
 gctgtcatc ttacaactct acttgagtat gtccctaacc ctgagcccc 350  
 cagcctggg gccagagtct ttgtccccg tgtgcgcatg tggtcagggt 400  
 cagcctctcc cagaagtgag atcatggaca aaaagggcaa atcacaggaa 450  
 gaaattaaat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500  
 gccgagacct gcaggagtgg tgccagggtc ttgaagtaac aagtttaaaa 550  
 tggtcagaga caatggaatg gaatctatta ggcaagaaca ggacattatg 600  
 aaataaggac aggtggactt ccaaaaacac aagtagaaat tctaacaatg 650  
 aaatatatta caggcaggtc acccactaac caaacaactg aagcgagagc 700  
 tgtggtcttg cttggtctca cagtgggcac agcggtaggc ggtcagtcac 750  
 gttgctgaac gacggagggt aaactcccca gccccaagaa aacctgtgtt 800  
 ggaagtaaca acaacctccc tgctcctggc accagccgtt ttggtcatgg 850  
 tgggccagct gcaaagcgtc ttccattctc tgggcagtgg tggccccgag 900  
 gctgtggcct ctcaagggtt ttctgtggac acgggcagca gagtgtgtcc 950  
 aggccagccc ccaagaatgc cctgctcctg acagcttggc caaccctgg 1000  
 tcagggcaga gggagttggg tgggtcaggc tctgggtca cctccatctc 1050





tggagataacc aacacatcca cccaggaggt ggtacaatac aactgggaga 300  
 ctgggggatga ccggttctcc ttccggagct tccggagtgg catgtggcta 350  
 tcctgtgagg aaactgtgga agaaccaggg gagagggtgcc gaagtttcat 400  
 tgaacttaca ccaccagcca agagagggtga gaaaggacta ctggaatttg 450  
 ccacgttgca aggcccatgt caccctactc tccgatttgg agggaagcgg 500  
 ttgatggaga aggcttccct cccctcccct cccttggggc tttgtggcaa 550  
 aaatcctatg gttatccctg ggaacgcaga tcacctacat cggacttcaa 600  
 ttcatcagct tcctcctgct actaacagac ttgctactca ctgggaaccc 650  
 tgcctgtggg ctcaaactga gcgcctttgc tgcgttttcc tctgtcctgt 700  
 caggctctcct ggggatgggtg gccacatga tgtattcaca agtcttccaa 750  
 gcgactgtca acttgggtcc agaagactgg agaccacatg tttggaatta 800  
 tggctgggcc ttctacatgg cctggctctc cttcacctgc tgcattggcg 850  
 cggctgtcac caccttcaac acgtacacca ggatgggtgct ggagttcaag 900  
 tgcaagcata gtaagagctt caaggaaaac ccgaactgcc taccacatca 950  
 ccatcagtgt ttccctcggc ggctgtcaag tgcagcccc accgtgggtc 1000  
 ctttgaccag ctaccaccag tatcataatc agcccatcca ctctgtctct 1050  
 gagggagtgc acttctactc cgagctgcgg aacaagggat ttcaaagagg 1100  
 gggcagccag gagctgaaag aagcagttag gtcattctgta gaggaagagc 1150  
 agtgtttaga gttaagcggg tttggggagt aggccttgagc cctaccttac 1200  
 acgtctgctg attatcaaca tgtgcttaag ccaacatccg tctcttgagc 1250  
 atggttttta gaggtacga ataaggctat gaataagggt tatctttaag 1300  
 tcctaaggga ttctgggtg ccactgctct cttttcctct acagctocat 1350  
 cttgtttcac ccacccaca tctcacacat ccagaattcc cttctttact 1400  
 gatagtttct gtgccaggtt ctgggctaaa ccatggagat aaaaagaaga 1450  
 gtaaaatata cttcccgacc ttaaggatct gaaa 1484

<210> 272  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 272  
 Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr  
 1 5 10 15  
 Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr  
 20 25 30  
 Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val

	35		40		45
Pro Lys Pro Leu Cys	50	Glu Lys Gly Leu Ala	55	Ala Lys Cys Phe	60
Met Pro Val Ser Leu	65	Asp Gly Asp Thr Asn	70	Thr Ser Thr Gln Glu	75
Val Val Gln Tyr Asn	80	Trp Glu Thr Gly Asp	85	Asp Arg Phe Ser Phe	90
Arg Ser Phe Arg Ser	95	Gly Met Trp Leu Ser	100	Cys Glu Glu Thr Val	105
Glu Glu Pro Gly Glu	110	Arg Cys Arg Ser Phe	115	Ile Glu Leu Thr Pro	120
Pro Ala Lys Arg Gly	125	Glu Lys Gly Leu Leu	130	Glu Phe Ala Thr Leu	135
Gln Gly Pro Cys His	140	Pro Thr Leu Arg Phe	145	Gly Gly Lys Arg Leu	150
Met Glu Lys Ala Ser	155	Leu Pro Ser Pro Pro	160	Leu Gly Leu Cys Gly	165
Lys Asn Pro Met Val	170	Ile Pro Gly Asn Ala	175	Asp His Leu His Arg	180
Thr Ser Ile His Gln	185	Leu Pro Pro Ala Thr	190	Asn Arg Leu Ala Thr	195
His Trp Glu Pro Cys	200	Leu Trp Ala Gln Thr	205	Glu Arg Leu Cys Cys	210
Cys Phe Leu Cys Pro	215	Val Arg Ser Pro Gly	220	Asp Gly Gly Pro His	225
Asp Val Phe Thr Ser	230	Leu Pro Ser Asp Cys	235	Gln Leu Gly Ser Arg	240
Arg Leu Glu Thr Thr	245	Cys Leu Glu Leu Trp	250	Leu Gly Leu Leu His	255
Gly Leu Ala Leu Leu	260	His Leu Leu His Gly	265	Val Gly Cys His His	270
Leu Gln His Val His	275	Gln Asp Gly Ala Gly	280	Val Gln Val Gln Ala	285

<210> 273  
 <211> 1158  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
 aactggaagg aaagaaagaa aggtcagctt tggcccagat gtggttaccc 50  
 cttggtctcc tgtctttatg tctttctcct cttcctattc tgtcatctcc 100  
 ctcacttaag tctcaggcct gtcagcagct cctgtggaca ttgccatccc 150  
 ctctggtagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

accaaccagg gtagtggcat ggagcaccgt aaccatctgt gcttctgtga 250  
 tctctatgac agagccactt ctccacctct gaaatgttcc ctgctctgaa 300  
 atctggcatg agatggcaca ggtgaccacg cagaagccac cagaatcttg 350  
 cctgccctat tcctcctccc aagtctgttc tcttattgtc aacctcagca 400  
 caacaggctg gcgccaatgg cattacagag aaagcaatct gtgtggctag 450  
 tgggcagatt accatgcaag cccaggaga aatggaggag cttttagtagc 500  
 acctccctgt cagccagtat taacatgtcc ccttccccct gccccgccgt 550  
 agattcagga cattcgcccc tgtgtgccac caaaccagga ctttccccct 600  
 ggcttggcat ccctggctct ctctggtac ccagcaagac gtctgttcca 650  
 gggcagtgtg gcatctttca agctccgtta ctatggcgat ggccatgatg 700  
 ttacaatccc acttgctga ataatcaagt gggaagggga agcagaggga 750  
 aatggggcca tgtgaatgca gctgctctgt tctccctacc ctgaggaaaa 800  
 accaaagggga agcaacagga acttctgcaa ctggttttta tcggaaagat 850  
 catcctgcct gcagatgctg ttgaaggggc acaagaaatg tagctggaga 900  
 agattgatga aagtgcaggt gtgtaaggaa atagaacagt ctgctgggag 950  
 tcagacctgg aattctgatt ccaaactctt tattactttg ggaagtcaact 1000  
 cagcctcccc gtagccatct ccagggtgac ggaaccaggt gtattacctg 1050  
 ctggaaccaa ggaaactaac aatgtaggtt actagtgaat accccaatgg 1100  
 tttctccaat tatgccatg ccacaaaaac aataaaacaa aattctctaa 1150  
 cactgaaa 1158

<210> 274  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
 Met Trp Leu Pro Leu Gly Leu Leu Ser Leu Cys Leu Ser Pro Leu 15  
 1 5 10  
 Pro Ile Leu Ser Ser Pro Ser Leu Lys Ser Gln Ala Cys Gln Gln 30  
 20 25 30  
 Leu Leu Trp Thr Leu Pro Ser Pro Leu Val Ala Phe Arg Ala Asn 45  
 35 40 45  
 Arg Thr Thr Tyr Val Met Asp Val Ser Thr Asn Gln Gly Ser Gly 60  
 50 55 60  
 Met Glu His Arg Asn His Leu Cys Phe Cys Asp Leu Tyr Asp Arg 75  
 65 70 75  
 Ala Thr Ser Pro Pro Leu Lys Cys Ser Leu Leu 85  
 80 85

<210> 275  
<211> 2694  
<212> DNA  
<213> Homo sapiens

<400> 275  
gtagcgcgtc ttgggtctcc cggtgcgcg tgctgcgcg gccgcctcgg 50  
gtcgtggagc caggagcgac gtcaccgcca tggcaggcat caaagctttg 100  
attagtttgt cctttggagg agcaatcgga ctgatgtttt tgatgcttgg 150  
atgtgccctt ccaatataca acaaatactg gccctctttt gttctatttt 200  
tttacatcct ttcacctatt ccatactgca tagcaagaag attagtggat 250  
gatacagatg ctatgagtaa cgcttgtaag gaacttgcca tctttcttac 300  
aacgggcatt gtctgtcag cttttggact ccctattgta tttgccagag 350  
cacatctgat tgagtgggga gcttgtgcac ttgttctcac aggaaacaca 400  
gtcatctttg caactatact aggccttttc ttggtctttg gaagcaatga 450  
cgacttcagc tggcagcagt ggtgaaaaga aattactgaa ctattgtcaa 500  
atggacttcc tgtcatttgt tggccattca cgcacacagg agatggggca 550  
gttaatgctg aatggtatag caagcctctt ggggggtattt taggtgctcc 600  
cttctcactt ttattgtaag catactattt tcacagagac ttgctgaagg 650  
attaaaagga ttttctcttt tggaaaagct tgactgattt cacacttacc 700  
tatagtatgc tttttgtggt gtctgtgta atttaaataat ttatgtgttt 750  
ttcctgttag gttgattttt tttggaatca atatgcaatg ttaaactt 800  
ttttaatgta atcatttgca ttggttagga attcagaatt ccgccggctc 850  
tattactggt caagtacatc ttttctctta aaattattta gcctccatta 900  
ttacaaaaaa ttataaaaat aagttttcag tcagtcagga tgacatcact 950  
cccaatgta tgcagacata cagacggttg gcatacgtta tagactgtat 1000  
actcagtgc aatatagctg catctataacc tcagaggggc caagtgttaa 1050  
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<210> 276

<211> 131

<212> PRT

<213> Homo sapiens

<400> 276

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<210> 278  
 <211> 522  
 <212> PRT  
 <213> Homo sapiens

<400> 278

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Arg	Pro	Ser	Gly	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala	Cys	Phe	Gln	20	25	30	
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys	35	40	45	
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala	50	55	60	
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	65	70	75	
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln	80	85	90	
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln	95	100	105	
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu	110	115	120	
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro	125	130	135	
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln	140	145	150	
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Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys	200	205	210	
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn	215	220	225	
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu	230	235	240	
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val	245	250	255	
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr	260	265	270	
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu	275	280	285	

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Trp	Asp	Cys	Gly	Arg	Asn	Val	Cys	Ala	Leu	Ala	Ser	Trp	Leu	Ser	320	325	330
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His	Leu	Cys	Glu	Asp	Gly	Ala	Glu	Pro	Thr	Ser	Gly	His	Leu	Leu	365	370	375
Ser	Ala	Val	Thr	Asn	Arg	Ser	Asp	Leu	Gly	Pro	Pro	Ala	Ser	Ser	380	385	390
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Phe	Glu	Pro	Ala	Thr	Val	Ala	Leu	Pro	Gly	Gly	Glu	His	Ala	Glu	410	415	420
Asn	Ala	Val	Gln	Ile	His	Lys	Val	Val	Thr	Gly	Thr	Met	Ala	Leu	425	430	435
Ile	Phe	Ser	Phe	Leu	Ile	Val	Val	Leu	Val	Leu	Tyr	Val	Ser	Trp	440	445	450
Lys	Cys	Phe	Pro	Ala	Ser	Leu	Arg	Gln	Leu	Arg	Gln	Cys	Phe	Val	455	460	465
Thr	Gln	Arg	Arg	Lys	Gln	Lys	Gln	Lys	Gln	Thr	Met	His	Gln	Met	470	475	480
Ala	Ala	Met	Ser	Ala	Gln	Glu	Tyr	Tyr	Val	Asp	Tyr	Lys	Pro	Asn	485	490	495
His	Ile	Glu	Gly	Ala	Leu	Val	Ile	Ile	Asn	Glu	Tyr	Gly	Ser	Cys	500	505	510
Thr	Cys	His	Gln	Gln	Pro	Ala	Arg	Glu	Cys	Glu	Val				515	520	

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<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

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<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

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<210> 281  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 281  
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 Asp Val Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly  
 35 40 45  
 Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val  
 50 55 60  
 Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly  
 65 70 75  
 Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val  
 80 85 90  
 Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg  
 95 100 105  
 Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser  
 110 115 120  
 Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val  
 125 130 135



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Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe					
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Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe					
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Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys					
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Leu Ala					

<210> 284  
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 <212> DNA  
 <213> Homo sapiens

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<210> 285







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<210> 287

<211> 255

<212> PRT

<213> Homo sapiens

<400> 287

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Val	Gly	Asp	Asp	Tyr	His	Ala	Trp	Asn	Ile	Asn	Tyr	Lys	Lys	Trp
			35						40					45
Glu	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Pro	Pro	Pro	Pro	Thr
			50						55					60
Pro	Val	Ser	Gly	Glu	Glu	Gly	Arg	Ala	Ala	Ala	Pro	Asp	Val	Ala
			65						70					75
Pro	Ala	Pro	Gly	Pro	Ala	Pro	Arg	Ala	Pro	Leu	Asp	Phe	Arg	Gly
			80						85					90
Met	Leu	Arg	Lys	Leu	Phe	Ser	Ser	His	Arg	Phe	Gln	Val	Ile	Ile
			95						100					105
Ile	Cys	Leu	Val	Val	Leu	Asp	Ala	Leu	Leu	Val	Leu	Ala	Glu	Leu
			110						115					120

Ile	Leu	Asp	Leu	Lys	Ile	Ile	Gln	Pro	Asp	Lys	Asn	Asn	Tyr	Ala
				125					130					135
Ala	Met	Val	Phe	His	Tyr	Met	Ser	Ile	Thr	Ile	Leu	Val	Phe	Phe
				140					145					150
Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser
				155					160					165
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val
				170					175					180
Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe
				185					190					195
Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala
				200					205					210
Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu
				215					220					225
Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala
				230					235					240
Lys	Ile	Gln	His	Leu	Glu	Phe	Ser	Cys	Ser	Glu	Lys	Pro	Leu	Asp
				245					250					255

<210> 288  
 <211> 3334  
 <212> DNA  
 <213> Homo sapiens

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 cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg 150  
 aagtcatttt tcaagctcag tgtcttcac cctcccagg aattctccac 200  
 ctaccgccag tggaagcaga aaattgtaca agctggagat aaggaccttg 250  
 atgggcagct agactttgaa gaatttgtcc attatctcca agatcatgag 300  
 aagaagctga ggctggtgtt taagattttg gacaaaaaga atgatggacg 350  
 cattgacgcy caggagatca tgcagtcctt gcgggacttg ggagtcaaga 400  
 tatctgaaca gcaggcagaa aaaattctca agagcatgga taaaaacggc 450  
 acgatgacca tcgactggaa cgagtggaga gactaccacc tcctccaccc 500  
 cgtggaaaac atccccgaga tcatoctcta ctggaagcat tccacgatct 550  
 ttgatgtggg tgagaatcta acgggtcccg atgagttcac agtggaggag 600  
 aggcagacgg ggatgtggtg gagacacctg gtggcaggag gtggggcagg 650  
 ggccgtatcc agaacctgca cggccccctt ggacaggctc aaggtgctca 700  
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atgagcagat caagcgcctt gttggtagtg accaggagac tctgaggatt 900  
cacgagaggc ttgtggcagg gtccttggca gggggccatcg ccagagacag 950  
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gccagtactc aggaatgctg gactgcgcca ggaggatcct ggccagagag 1050  
ggggtggccg ccttctacaa aggctatgtc cccaacatgc tgggcatcat 1100  
cccctatgcc ggcatcgacc ttgcagtcta cgagacgctc aagaatgcct 1150  
ggctgcagca ctatgcagtg aacagcgcgg accccggcgt gtttgtgctc 1200  
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cccagctgtg agcatcagct acgtggtcta cgagaacctg aagatcaccc 1450  
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tggggaggga aggaaaaggt gttggaggcc ttaattatgg actgttggga 2350

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 tttatttgaa cagagttatg tcctaactat ttttatagat ttgtttaatt 2600  
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 ggggggcctt gggccgctgc agtcacatct gtccagagaa attccttttg 2750  
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 gactgggggc gtggagagag agggaggaac ctcaataacc ttgaagggtg 2900  
 aatccagtta tttcctgcgc tgcgagggtt tctttatttc actcttttct 2950  
 gaatgtcaag gcagtgaggt gcctctcact gtgaatttgt ggtgggcggg 3000  
 ggctggagga gaggggtggg ggctggctcc gtccctccca gccttctgct 3050  
 gcccttgctt aacaatgccg gccaaactggc gacctcacgg ttgcacttcc 3100  
 attccaccag aatgacctga tgaggaaatc ttcaatagga tgcaaagatc 3150  
 aatgcaaaaa ttgttatata tgaacatata actggagtcg tcaaaaagca 3200  
 aattaagaaa gaattggacg ttagaagttg tcatttaaag cagccttcta 3250  
 ataaagttgt ttcaaagctg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3300  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 3334

<210> 289  
 <211> 469  
 <212> PRT  
 <213> Homo sapiens

<400> 289  
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 Lys Ser Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe  
 35 40 45  
 Ser Thr Tyr Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp  
 50 55 60  
 Lys Asp Leu Asp Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr  
 65 70 75  
 Leu Gln Asp His Glu Lys Lys Leu Arg Leu Val Phe Lys Ile Leu  
 80 85 90

Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	
				95					100					105	
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	
				110					115					120	
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp	
				125					130					135	
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn	
				140					145					150	
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp	
				155					160					165	
Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu	
				170					175					180	
Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly	
				185					190					195	
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu	
				200					205					210	
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly	
				215					220					225	
Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg	
				230					235					240	
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	
				245					250					255	
Glu	Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Ile	Lys	Arg	Leu	
				260					265					270	
Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	
				275					280					285	
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	
				290					295					300	
Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	
				305					310					315	
Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu	
				320					325					330	
Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly	
				335					340					345	
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	
				350					355					360	
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro	
				365					370					375	
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys	
				380					385					390	
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	
				395					400					405	

Gln	Ala	Gln	Ala	Ser	Ile	Glu	Gly	Ala	Pro	Glu	Val	Thr	Met	Ser
				410					415					420
Ser	Leu	Phe	Lys	His	Ile	Leu	Arg	Thr	Glu	Gly	Ala	Phe	Gly	Leu
				425					430					435
Tyr	Arg	Gly	Leu	Ala	Pro	Asn	Phe	Met	Lys	Val	Ile	Pro	Ala	Val
				440					445					450
Ser	Ile	Ser	Tyr	Val	Val	Tyr	Glu	Asn	Leu	Lys	Ile	Thr	Leu	Gly
				455					460					465

Val Gln Ser Arg

<210> 290  
 <211> 1658  
 <212> DNA  
 <213> Homo sapiens

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 gcatcatcat tattctggct ggagcaattg cactcatcat tggctttggt 150  
 atttcagggg gacactccat cacagtcact actgtcgccct cagctgggaa 200  
 cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250  
 tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 300  
 catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatggt 350  
 cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400  
 ctttgccggt gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450  
 tatatcatca cttctaaagg caaggggaat gctaaccttg agtataaaac 500  
 tggagccttc agcatgccgg aagtgaatgt ggactataat gccagctcag 550  
 agacottgog gtgtgaggct ccccgatggt tccccagcc cacagtgggtc 600  
 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650  
 cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc 700  
 tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750  
 attgccaaag caacagggga tatcaaagt acagaatcgg agatcaaaag 800  
 gcggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850  
 ctttctttgc catcagctgg gcacttctgc ctctcagccc ttacctgatg 900  
 ctaaaataat gtgccttggc caaaaaaaag catgcaaagt cattgttaca 950  
 acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000  
 ttctgggagg aaatgaattc atatctagaa gtctggagt agcaaacaag 1050

agcaagaaac aaaaagaagc caaaagcaga aggcctccaat atgaacaaga 1100  
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 actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 1200  
 gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtgag 1250  
 aggacaggat agtgcattgtt ctttgtctct gaatttttag ttatatgtgc 1300  
 tgtaatgttg ctctgaggaa gcccttgaa agtctatccc aacatatcca 1350  
 catcttatat tccacaaatt aagctgtagt atgtacccta agacgtgct 1400  
 aattgactgc cacttcgcaa ctcagggcg gctgcatttt agtaatgggt 1450  
 caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500  
 ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa 1550  
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 ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
 aaaaaaaaa 1658

<210> 291  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 291  
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 20 25 30  
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala  
 35 40 45  
 Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro  
 50 55 60  
 Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly  
 65 70 75  
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu  
 80 85 90  
 Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala  
 95 100 105  
 Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val  
 110 115 120  
 Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser  
 125 130 135  
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe  
 140 145 150  
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr









<213> Homo sapiens

<400> 295

Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala  
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20 25 30  
Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn  
35 40 45  
Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro  
50 55 60  
Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser  
65 70 75  
Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu  
80 85 90  
Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys  
95 100 105  
Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser  
110 115 120  
Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser  
125 130 135  
Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val  
140 145 150  
Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu  
155 160 165  
Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe  
170 175 180  
Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys  
185 190 195  
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro  
200 205 210  
Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu  
215 220 225  
Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro  
230 235

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

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ccagcccat ggtccccgcc gccggcgcgc tgctgtgggt cctgctgctg 150

aatctgggtc cccgggcggc gggggcccaa ggcctgaccc agactccgac 200  
cgaaatgcag cgggtcagtt tacgctttgg gggcccatg acccgagct 250  
accggagcac cgcccgact ggtcttcccc ggaagacaag gataatccta 300  
gaggacgaga atgatgccat ggccgacgcc gaccgcctgg ctggaccagc 350  
ggctgccgag ctcttgccg ccacgggtgc caccggcttt agccggtcgt 400  
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gccggaaagg atagcaccag cagagagctt cccagtgcga ctccaatac 500  
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<210> 297

<211> 341

<212> PRT

<213> Homo sapiens

<400> 297

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20 25 30

Thr Glu Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr  
35 40 45

Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr  
50 55 60

Arg Ile Ile Leu Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp

65										70					75				
Arg	Leu	Ala	Gly	Pro	Ala	Ala	Ala	Glu	Leu	Leu	Ala	Ala	Thr	Val					
				80					85					90					
Ser	Thr	Gly	Phe	Ser	Arg	Ser	Ser	Ala	Ile	Asn	Glu	Glu	Asp	Gly					
				95					100					105					
Ser	Ser	Glu	Glu	Gly	Val	Val	Ile	Asn	Ala	Gly	Lys	Asp	Ser	Thr					
				110					115					120					
Ser	Arg	Glu	Leu	Pro	Ser	Ala	Thr	Pro	Asn	Thr	Ala	Gly	Ser	Ser					
				125					130					135					
Ser	Thr	Arg	Phe	Ile	Ala	Asn	Ser	Gln	Glu	Pro	Glu	Ile	Arg	Leu					
				140					145					150					
Thr	Ser	Ser	Leu	Pro	Arg	Ser	Pro	Gly	Arg	Ser	Thr	Glu	Asp	Leu					
				155					160					165					
Pro	Gly	Ser	Gln	Ala	Thr	Leu	Ser	Gln	Trp	Ser	Thr	Pro	Gly	Ser					
				170					175					180					
Thr	Pro	Ser	Arg	Trp	Pro	Ser	Pro	Ser	Pro	Thr	Ala	Met	Pro	Ser					
				185					190					195					
Pro	Glu	Asp	Leu	Arg	Leu	Val	Leu	Met	Pro	Trp	Gly	Pro	Trp	His					
				200					205					210					
Cys	His	Cys	Lys	Ser	Gly	Thr	Met	Ser	Arg	Ser	Arg	Ser	Gly	Lys					
				215					220					225					
Leu	His	Gly	Leu	Ser	Gly	Arg	Leu	Arg	Val	Gly	Ala	Leu	Ser	Gln					
				230					235					240					
Leu	Arg	Thr	Glu	His	Lys	Pro	Cys	Thr	Tyr	Gln	Gln	Cys	Pro	Cys					
				245					250					255					
Asn	Arg	Leu	Arg	Glu	Glu	Cys	Pro	Leu	Asp	Thr	Ser	Leu	Cys	Thr					
				260					265					270					
Asp	Thr	Asn	Cys	Ala	Ser	Gln	Ser	Thr	Thr	Ser	Thr	Arg	Thr	Thr					
				275					280					285					
Thr	Thr	Pro	Phe	Pro	Thr	Ile	His	Leu	Arg	Ser	Ser	Pro	Ser	Leu					
				290					295					300					
Pro	Pro	Ala	Ser	Pro	Cys	Pro	Ala	Leu	Ala	Phe	Trp	Lys	Arg	Val					
				305					310					315					
Arg	Ile	Gly	Leu	Glu	Asp	Ile	Trp	Asn	Ser	Leu	Ser	Ser	Val	Phe					
				320					325					330					
Thr	Glu	Met	Gln	Pro	Ile	Asp	Arg	Asn	Gln	Arg									
				335					340										

<210> 298  
 <211> 2692  
 <212> DNA  
 <213> Homo sapiens

<400> 298  
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 cgaccgtgag cgggtgtacc gcgactgcgt actgcagtgc gaagagcaga 150  
 actgctctgg gggcgctctg aatcacttcc gctcccgccca gccaatctac 200  
 atgagtctag caggctggac ctgtcgggac gactgtaagt atgagtgtat 250  
 gtgggtcacc gttgggctct acctccagga aggtcacaaa gtgcctcagt 300  
 tccatggcaa gtggcccttc tcccggttcc tgttctttca agagccggca 350  
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<210> 299  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 299  
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 20 25 30  
 Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala  
 35 40 45  
 Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala  
 50 55 60  
 Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val  
 65 70 75



Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys Val Pro Gln Phe  
 80 85 90  
 His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe Gln Glu Pro  
 95 100 105  
 Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu Ala Ser Leu Val  
 110 115 120  
 Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro Met  
 125 130 135  
 Tyr His Thr Cys Val Ala Phe Ala Trp Val Ser Leu Asn Ala Trp  
 140 145 150  
 Phe Trp Ser Thr Val Phe His Thr Arg Asp Thr Asp Leu Thr Glu  
 155 160 165  
 Lys Met Asp Tyr Phe Cys Ala Ser Thr Val Ile Leu His Ser Ile  
 170 175 180  
 Tyr Leu Cys Cys Val Arg Thr Val Gly Leu Gln His Pro Ala Val  
 185 190 195  
 Val Ser Ala Phe Arg Ala Leu Leu Leu Leu Met Leu Thr Val His  
 200 205 210  
 Val Ser Tyr Leu Ser Leu Ile Arg Phe Asp Tyr Gly Tyr Asn Leu  
 215 220 225  
 Val Ala Asn Val Ala Ile Gly Leu Val Asn Val Val Trp Trp Leu  
 230 235 240  
 Ala Trp Cys Leu Trp Asn Gln Arg Arg Leu Pro His Val Arg Lys  
 245 250 255  
 Cys Val Val Val Val Leu Leu Leu Gln Gly Leu Ser Leu Leu Glu  
 260 265 270  
 Leu Leu Asp Phe Pro Pro Leu Phe Trp Val Leu Asp Ala His Ala  
 275 280 285  
 Ile Trp His Ile Ser Thr Ile Pro Val His Val Leu Phe Phe Ser  
 290 295 300  
 Phe Leu Glu Asp Asp Ser Leu Tyr Leu Leu Lys Glu Ser Glu Asp  
 305 310 315  
 Lys Phe Lys Leu Asp  
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<210> 300

<211> 1674

<212> DNA

<213> Homo sapiens

<400> 300

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cctcagtcac cagaacctga aggagtttgc cctgaccaac ccagagaaga 200  
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<210> 301



290	295	300
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305	310	315
Leu Arg Thr Leu Val Gln Glu Lys Gly	Thr Glu Val Leu Ala Val	
320	325	330
Arg Val Val Thr Leu Leu Tyr Asp Leu	Val Thr Glu Lys Met Phe	
335	340	345
Ala Glu Glu Glu Ala Glu Leu Thr Gln	Glu Met Ser Pro Glu Lys	
350	355	360
Leu Gln Gln Tyr Arg Gln Val His Leu	Leu Pro Gly Leu Trp Glu	
365	370	375
Gln Gly Trp Cys Glu Ile Thr Ala His	Leu Leu Ala Leu Pro Glu	
380	385	390
His Asp Ala Arg Glu Lys Val Leu Gln	Thr Leu Gly Val Leu Leu	
395	400	405
Thr Thr Cys Arg Asp Arg Tyr Arg Gln	Asp Pro Gln Leu Gly Arg	
410	415	420
Thr Leu Ala Ser Leu Gln Ala Glu Tyr	Gln Val Leu Ala Ser Leu	
425	430	435
Glu Leu Gln Asp Gly Glu Asp Glu Gly	Tyr Phe Gln Glu Leu Leu	
440	445	450
Gly Ser Val Asn Ser Leu Leu Lys Glu	Leu Arg	
455	460	

<210> 302  
 <211> 2136  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
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 tcccatattgc ctgtcctggt caggccccca ccccccttcc cacctgacca 200  
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 tcatactggt cgcaggggca tttttctggc tggctccct gctcctggcc 350  
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 gggttagcat cgctgagtga ggacggaaga tcacccatct ccatccgcca 550

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 catggagact caccctatta cttcctgact tcagcctttc tgacagcagc 700  
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 ggtggagtgt cccatccttt taatcaaggt gattgtgatt ttgactaata 2050  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 303

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Arg	Val	Ile	Ile	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	50	55	60	
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	95	100	105	
Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	110	115	120	
Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile	125	130	135	
Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His	140	145	150	
Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala	155	160	165	
Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	Phe	Asp	170	175	180	
Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	Gly	185	190	195	
Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	200	205	210	
Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	215	220	225	
Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln	230	235	240	
Arg	Ser	Leu	Leu	Cys	Lys	Asp									245			

<210> 304  
 <211> 240  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> unsure  
<222> 108, 123, 126, 154, 198, 206, 217  
<223> unknown base

<400> 304  
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ccttcggnat catcagtggg gtnttntctg ttatcaatat tttggctgat 150  
gcanttgggc caggtgtggg tgggatccat ggagactcac cctattantt 200  
cctganttca gccttntga cagcagccat tatcctgctc 240

<210> 305  
<211> 378  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332  
<223> unknown base

<400> 305  
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<210> 306  
<211> 655  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1, 22, 129, 133, 184  
<223> unknown base

<400> 306  
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gcgttgccac cccacgogga ctccccagnt gngcgccct tccatttgc 150  
ctgtcctggt caggccccca ccccccttc cacntgacca gccatggggg 200  
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cttttcttga tcaactgtggc tggggacccg cttcgcgtta tcatcctggt 300  
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 ggcctcctga tttttggtgc tgctgtctct gtccttctac aggaggtggt 450  
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 cgctgagtga ggacggaaga taccatctt ccatccgcca gatggcctat 550  
 gtttctggtc tctccttcgg tatcatcagt ggtgtcttct ctgttatcaa 600  
 tattttggct gatgcacttg ggccaggtgt ggttgggatc catggagact 650  
 cacc 655

<210> 307  
 <211> 650  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 52, 89, 128  
 <223> unknown base

<400> 307  
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 tgtttctggt ctctccttcg gtatcatcag tgggtgtctt tctgttatca 600  
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<210> 308  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 308  
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accgtgtctc tctagttgaa ccctgggaac aatttccaaa actgtccagg 1450  
gcgggggttg cgtctcaatc tcctggggc actttcatcc tcaagctcag 1500  
ggcccatccc ttctctgcag ctctgaccca aatttagtcc cagaaataaa 1550  
ctgagaagtg gaaaaaaaaa 1570

<210> 309



<210> 310  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 310  
 tcctgtgacc acccctctaa cacc 24

<210> 311  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 311  
 ctggaacatc tgctgccag attc 24

<210> 312  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 312  
 gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313  
 <211> 3010  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 atggtcaacg accggtggaa gaccatgggc ggcgctgccc aacttgagga 50  
 ccggccgcgc gacaagcgc agcgcccgag ctgcggctac gtgctgtgca 100  
 ccgtgctgct ggccctggct gtgctgctgg ctgtagctgt caccggtgcc 150  
 gtgctcttcc tgaaccacgc ccacgcgcgc ggcacggcgc cccacactgt 200  
 cgtcagcact ggggctgcca gcgccaacag cgccctggtc actgtggaaa 250  
 gggcggacag ctgcacctc agcatcctca ttgaccgcgc ctgccccgac 300  
 ctcaccgaca gcttcgcacg cctggagagc gccaggcct cgggtgctgca 350  
 ggcgctgaca gagcaccagg ccagccacg gctggtgggc gaccaggagc 400  
 aggagctgct ggacacgctg gcgaccagc tgccccggct gctggcccga 450  
 gcctcagagc tgcagacgga gtgcatgggg ctgcggaagg ggcattggac 500  
 gctgggccag ggcctcagcg ccctgcagag tgagcagggc cgcctcatcc 550





Ala Arg Leu Glu Ser	Ala Gln Ala Ser	Val Leu Gln Ala Leu Thr	110	115	120
Glu His Gln Ala Gln	Pro Arg Leu Val	Gly Asp Gln Glu Gln Glu	125	130	135
Leu Leu Asp Thr Leu	Ala Asp Gln Leu	Pro Arg Leu Leu Ala Arg	140	145	150
Ala Ser Glu Leu Gln	Thr Glu Cys Met	Gly Leu Arg Lys Gly His	155	160	165
Gly Thr Leu Gly Gln	Gly Leu Ser Ala	Leu Gln Ser Glu Gln Gly	170	175	180
Arg Leu Ile Gln Leu	Leu Ser Glu Ser	Gln Gly His Met Ala His	185	190	195
Leu Val Asn Ser Val	Ser Asp Ile Leu	Asp Ala Leu Gln Arg Asp	200	205	210
Arg Gly Leu Gly Arg	Pro Arg Asn Lys	Ala Asp Leu Gln Arg Ala	215	220	225
Pro Ala Arg Gly Thr	Arg Pro Arg Gly	Cys Ala Thr Gly Ser Arg	230	235	240
Pro Arg Asp Cys Leu	Asp Val Leu Leu	Ser Gly Gln Gln Asp Asp	245	250	255
Gly Val Tyr Ser Val	Phe Pro Thr His	Tyr Pro Ala Gly Phe Gln	260	265	270
Val Tyr Cys Asp Met	Arg Thr Asp Gly	Gly Gly Trp Thr Val Phe	275	280	285
Gln Arg Arg Glu Asp	Gly Ser Val Asn	Phe Phe Arg Gly Trp Asp	290	295	300
Ala Tyr Arg Asp Gly	Phe Gly Arg Leu	Thr Gly Glu His Trp Leu	305	310	315
Gly Leu Lys Arg Ile	His Ala Leu Thr	Thr Gln Ala Ala Tyr Glu	320	325	330
Leu His Val Asp Leu	Glu Asp Phe Glu	Asn Gly Thr Ala Tyr Ala	335	340	345
Arg Tyr Gly Ser Phe	Gly Val Gly Leu	Phe Ser Val Asp Pro Glu	350	355	360
Glu Asp Gly Tyr Pro	Leu Thr Val Ala	Asp Tyr Ser Gly Thr Ala	365	370	375
Gly Asp Ser Leu Leu	Lys His Ser Gly	Met Arg Phe Thr Thr Lys	380	385	390
Asp Arg Asp Ser Asp	His Ser Glu Asn	Asn Cys Ala Ala Phe Tyr	395	400	405
Arg Gly Ala Trp Trp	Tyr Arg Asn Cys	His Thr Ser Asn Leu Asn	410	415	420

Gly	Gln	Tyr	Leu	Arg	Gly	Ala	His	Ala	Ser	Tyr	Ala	Asp	Gly	Val
				425					430					435
Glu	Trp	Ser	Ser	Trp	Thr	Gly	Trp	Gln	Tyr	Ser	Leu	Lys	Phe	Ser
				440					445					450
Glu	Met	Lys	Ile	Arg	Pro	Val	Arg	Glu	Asp	Arg				
				455					460					

<210> 315  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 315  
 cacacgtcca acctcaatgg gcag 24

<210> 316  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 316  
 gaccagcagg gccaaaggaca agg 23

<210> 317  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 317  
 gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318  
 <211> 1841  
 <212> DNA  
 <213> Homo sapiens

<400> 318  
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 ggcaatccga ccacatttca ctctcaccgc ttaggaatc cagatgcagg 150  
 ccaagtacag cagcagcagg gacatgctgg atgatgatgg ggacaccacc 200  
 atgagcctgc atttctcaagc ctctgccaca actcggcatc cagagccccg 250  
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<400> 319

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1 5 10 15  
Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr  
20 25 30  
Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser  
35 40 45  
Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val  
50 55 60  
Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr  
65 70 75  
Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu  
80 85 90  
Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val  
95 100 105  
Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys  
110 115 120  
Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser  
125 130 135  
Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln  
140 145 150  
Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys  
155 160 165  
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp  
170 175 180  
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser  
185 190 195  
Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu  
200 205 210  
Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile  
215 220 225  
Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu  
230 235 240  
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys  
245 250 255  
Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His  
260 265 270  
Val Pro Pro Glu Thr Leu Gly Glu Gly Asp  
275 280

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

<220>  
<221> unsure  
<222> 59, 95, 149, 331, 364, 438, 446  
<223> unknown base

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cttttgccac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150  
cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200  
ggtgctgctg atagggctgg cagccctggg gcttttgttt tttcagtact 250  
accagctctc caatactggg caagacacca tttctcaa at ggaagaaaga 300  
ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaataataa 350  
gcttgacaga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400  
ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450  
atacacacac cacttccc 468

<210> 321  
<211> 23  
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<400> 321  
atgcaggcca agtacagcag cac 23

<210> 322  
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<400> 322  
catgctgacg acttctctgca agc 23

<210> 323  
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<400> 323  
ccacacagtc tctgcttctt ggg 23

<210> 324  
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<400> 324  
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<210> 325  
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<212> DNA  
<213> Homo sapiens

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gccgagcgca agaaccctgc gcagcccaga gcagctgctg gaggggaatc 50  
gaggcgcggc tccggggatt cggctcgggc cgctggctct gctctgcggg 100  
gagggagcgg gcccgccgcg ggggcccgag cctccggat ccgccccctc 150  
cccgtcccg cccctcggga gactcctctg gctgctctgg gggttcgccg 200  
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gagctgagga gggggcatct cccaacttct cccttttggga ccctgccgaa 2950

gctccctgcc ttttaataaac tggccaagtg tggaaaaa 2988

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<211> 775

<212> PRT

<213> Homo sapiens

<400> 326

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Val	Ala	Val	Gly	Ile	Ser	Leu	Gly	Phe	Thr	Leu	Ser	Leu	Leu	Ser	
				20					25					30	
Val	Thr	Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro	
				35					40					45	
Gly	Asp	Ser	Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg	
				50					55					60	
Arg	Pro	Asn	Ser	Val	Gln	Pro	Gly	Ala	Glu	Arg	Glu	Lys	Pro	Gly	
				65					70					75	
Ala	Gly	Glu	Gly	Ala	Gly	Glu	Asn	Trp	Glu	Pro	Arg	Val	Leu	Pro	
				80					85					90	
Tyr	His	Pro	Ala	Gln	Pro	Gly	Gln	Ala	Ala	Lys	Lys	Ala	Val	Arg	
				95					100					105	
Thr	Arg	Tyr	Ile	Ser	Thr	Glu	Leu	Gly	Ile	Arg	Gln	Arg	Leu	Leu	
				110					115					120	
Val	Ala	Val	Leu	Thr	Ser	Gln	Thr	Thr	Leu	Pro	Thr	Leu	Gly	Val	
				125					130					135	
Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg	Leu	Glu	Arg	Val	Val	Phe	
				140					145					150	
Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Ala	Pro	Pro	Gly	Met	Ala	Val	
				155					160					165	
Val	Thr	Leu	Gly	Glu	Glu	Arg	Pro	Ile	Gly	His	Leu	His	Leu	Ala	
				170					175					180	
Leu	Arg	His	Leu	Leu	Glu	Gln	His	Gly	Asp	Asp	Phe	Asp	Trp	Phe	
				185					190					195	
Phe	Leu	Val	Pro	Asp	Thr	Thr	Tyr	Thr	Glu	Ala	His	Gly	Leu	Ala	
				200					205					210	
Arg	Leu	Thr	Gly	His	Leu	Ser	Leu	Ala	Ser	Ala	Ala	His	Leu	Tyr	
				215					220					225	
Leu	Gly	Arg	Pro	Gln	Asp	Phe	Ile	Gly	Gly	Glu	Pro	Thr	Pro	Gly	
				230					235					240	
Arg	Tyr	Cys	His	Gly	Gly	Phe	Gly	Val	Leu	Leu	Ser	Arg	Met	Leu	
				245					250					255	
Leu	Gln	Gln	Leu	Arg	Pro	His	Leu	Glu	Gly	Cys	Arg	Asn	Asp	Ile	
				260					265					270	

Val	Ser	Ala	Arg	Pro 275	Asp	Glu	Trp	Leu	Gly 280	Arg	Cys	Ile	Leu	Asp 285
Ala	Thr	Gly	Val	Gly 290	Cys	Thr	Gly	Asp	His 295	Glu	Gly	Val	His	Tyr 300
Ser	His	Leu	Glu	Leu 305	Ser	Pro	Gly	Glu	Pro 310	Val	Gln	Glu	Gly	Asp 315
Pro	His	Phe	Arg	Ser 320	Ala	Leu	Thr	Ala	His 325	Pro	Val	Arg	Asp	Pro 330
Val	His	Met	Tyr	Gln 335	Leu	His	Lys	Ala	Phe 340	Ala	Arg	Ala	Glu	Leu 345
Glu	Arg	Thr	Tyr	Gln 350	Glu	Ile	Gln	Glu	Leu 355	Gln	Trp	Glu	Ile	Gln 360
Asn	Thr	Ser	His	Leu 365	Ala	Val	Asp	Gly	Asp 370	Arg	Ala	Ala	Ala	Trp 375
Pro	Val	Gly	Ile	Pro 380	Ala	Pro	Ser	Arg	Pro 385	Ala	Ser	Arg	Phe	Glu 390
Val	Leu	Arg	Trp	Asp 395	Tyr	Phe	Thr	Glu	Gln 400	His	Ala	Phe	Ser	Cys 405
Ala	Asp	Gly	Ser	Pro 410	Arg	Cys	Pro	Leu	Arg 415	Gly	Ala	Asp	Arg	Ala 420
Asp	Val	Ala	Asp	Val 425	Leu	Gly	Thr	Ala	Leu 430	Glu	Glu	Leu	Asn	Arg 435
Arg	Tyr	His	Pro	Ala 440	Leu	Arg	Leu	Gln	Lys 445	Gln	Gln	Leu	Val	Asn 450
Gly	Tyr	Arg	Arg	Phe 455	Asp	Pro	Ala	Arg	Gly 460	Met	Glu	Tyr	Thr	Leu 465
Asp	Leu	Gln	Leu	Glu 470	Ala	Leu	Thr	Pro	Gln 475	Gly	Gly	Arg	Arg	Pro 480
Leu	Thr	Arg	Arg	Val 485	Gln	Leu	Leu	Arg	Pro 490	Leu	Ser	Arg	Val	Glu 495
Ile	Leu	Pro	Val	Pro 500	Tyr	Val	Thr	Glu	Ala 505	Ser	Arg	Leu	Thr	Val 510
Leu	Leu	Pro	Leu	Ala 515	Ala	Ala	Glu	Arg	Asp 520	Leu	Ala	Pro	Gly	Phe 525
Leu	Glu	Ala	Phe	Ala 530	Thr	Ala	Ala	Leu	Glu 535	Pro	Gly	Asp	Ala	Ala 540
Ala	Ala	Leu	Thr	Leu 545	Leu	Leu	Leu	Tyr	Glu 550	Pro	Arg	Gln	Ala	Gln 555
Arg	Val	Ala	His	Ala 560	Asp	Val	Phe	Ala	Pro 565	Val	Lys	Ala	His	Val 570
Ala	Glu	Leu	Glu	Arg 575	Arg	Phe	Pro	Gly	Ala 580	Arg	Val	Pro	Trp	Leu 585

Ser	Val	Gln	Thr	Ala	Ala	Pro	Ser	Pro	Leu	Arg	Leu	Met	Asp	Leu	590	595	600
Leu	Ser	Lys	Lys	His	Pro	Leu	Asp	Thr	Leu	Phe	Leu	Leu	Ala	Gly	605	610	615
Pro	Asp	Thr	Val	Leu	Thr	Pro	Asp	Phe	Leu	Asn	Arg	Cys	Arg	Met	620	625	630
His	Ala	Ile	Ser	Gly	Trp	Gln	Ala	Phe	Phe	Pro	Met	His	Phe	Gln	635	640	645
Ala	Phe	His	Pro	Gly	Val	Ala	Pro	Pro	Gln	Gly	Pro	Gly	Pro	Pro	650	655	660
Glu	Leu	Gly	Arg	Asp	Thr	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ala	Ser	665	670	675
Glu	Ala	Cys	Phe	Tyr	Asn	Ser	Asp	Tyr	Val	Ala	Ala	Arg	Gly	Arg	680	685	690
Leu	Ala	Ala	Ala	Ser	Glu	Gln	Glu	Glu	Glu	Leu	Leu	Glu	Ser	Leu	695	700	705
Asp	Val	Tyr	Glu	Leu	Phe	Leu	His	Phe	Ser	Ser	Leu	His	Val	Leu	710	715	720
Arg	Ala	Val	Glu	Pro	Ala	Leu	Leu	Gln	Arg	Tyr	Arg	Ala	Gln	Thr	725	730	735
Cys	Ser	Ala	Arg	Leu	Ser	Glu	Asp	Leu	Tyr	His	Arg	Cys	Leu	Gln	740	745	750
Ser	Val	Leu	Glu	Gly	Leu	Gly	Ser	Arg	Thr	Gln	Leu	Ala	Met	Leu	755	760	765
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<210> 327  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 327  
 tggaaggctg ccgcaacgac aatc 24

<210> 328  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 329  
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<212> DNA  
<213> Artificial Sequence

<220>  
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atggctcagt gtgcagacag 20

<210> 330  
<211> 24  
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gcatgctgct ccgtgaagta gtcc 24

<210> 331  
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<212> DNA  
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<400> 331  
atgcatggga aagaaggcct gccc 24

<210> 332  
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<400> 332  
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<210> 333  
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<212> DNA  
<213> Homo sapiens

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gctttttaga agcttgattt cctttgaaga tgaaagacta gcggaagctc 200  
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gtatccaccc aaatgtcacc gatttcttcc tatgcaggaa atgagcagac 300  
ccatcaataa gaaatttctc agcctggccg aaaatggttg gccccacgaa 350  
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Glu Asp Glu

<210> 335  
<211> 442  
<212> DNA  
<213> Homo sapiens

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aggactgtgg tcgccccgtc cgctgtggcg ggaaagcggc cccagaacc 150  
gaccacaccg tggcaagagg acccagaacc cgaggacgaa aacttgatg 200  
agaagaacc agactcccat ggttatgaca aggaccccg tttggacgct 250  
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tggcagcacc tttgtggcct atctgcctga ctacaggatg aaagagtgg 350  
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<210> 336  
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<220>  
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<400> 336  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 337  
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<210> 338  
<211> 40  
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<220>  
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<400> 338  
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<210> 339  
<211> 2162  
<212> DNA

<213> Homo sapiens

<400> 339

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tcatacccc gctgccttcc ggggacgtag ccgccacatt ccagttccgc 150  
acgcgctggg attcggagct tcagcgggaa ggagtgtccc attacaggct 200  
ctttcccaaa gccctggggc agctgatctc caagtattct ctacgggagc 250  
tgcacctgtc attcacacaa ggcttttgga ggacccgata ctgggggcca 300  
cccttcctgc agggcccatc aggtgcagag ctgtgggtct ggttccaaga 350  
cactgtcact gatgtggata aatcttgaa ggagctcagt aatgtcctct 400  
cagggatctt ctgcgcctct ctcaacttca tcgactccac caacacagtc 450  
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ctactttctg cgctatgctg tgctgccgcg ggaggtggtc tgcaccgaaa 550  
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cctgggagct gaggcagacc ctgtcagttg tatttgatgc cttcatcacg 750  
gggcagggaa agaaagactg gtccctcttc cggatgttct cccgaaccct 800  
cacggagccc tgccccctgg cttcagagag ccgagtctat gtggacatca 850  
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actacatata aggacgtcat cctaggcact cggaagacct atgccatcta 950  
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gagcacactg ctgtacaaca cccaccata ccgggccttc ccggtgctgc 1150  
tgctggacac cgtaccctgg tatctgcggc tgtatgtgca caccctcacc 1200  
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tgcccaggac cggctgcaac cccacctcct ggagatgctg attcagctgc 1300  
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Ala	Ser	Phe	Lys	Pro	Leu	Gly	Leu	Ala	Asn	Asp	Thr	Asp	His	Tyr	155	160	165
Phe	Leu	Arg	Tyr	Ala	Val	Leu	Pro	Arg	Glu	Val	Val	Cys	Thr	Glu	170	175	180
Asn	Leu	Thr	Pro	Trp	Lys	Lys	Leu	Leu	Pro	Cys	Ser	Ser	Lys	Ala	185	190	195
Gly	Leu	Ser	Val	Leu	Leu	Lys	Ala	Asp	Arg	Leu	Phe	His	Thr	Ser	200	205	210
Tyr	His	Ser	Gln	Ala	Val	His	Ile	Arg	Pro	Val	Cys	Arg	Asn	Ala	215	220	225
Arg	Cys	Thr	Ser	Ile	Ser	Trp	Glu	Leu	Arg	Gln	Thr	Leu	Ser	Val	230	235	240
Val	Phe	Asp	Ala	Phe	Ile	Thr	Gly	Gln	Gly	Lys	Lys	Asp	Trp	Ser	245	250	255
Leu	Phe	Arg	Met	Phe	Ser	Arg	Thr	Leu	Thr	Glu	Pro	Cys	Pro	Leu	260	265	270
Ala	Ser	Glu	Ser	Arg	Val	Tyr	Val	Asp	Ile	Thr	Thr	Tyr	Asn	Gln	275	280	285
Asp	Asn	Glu	Thr	Leu	Glu	Val	His	Pro	Pro	Pro	Thr	Thr	Thr	Tyr	290	295	300
Gln	Asp	Val	Ile	Leu	Gly	Thr	Arg	Lys	Thr	Tyr	Ala	Ile	Tyr	Asp	305	310	315
Leu	Leu	Asp	Thr	Ala	Met	Ile	Asn	Asn	Ser	Arg	Asn	Leu	Asn	Ile	320	325	330
Gln	Leu	Lys	Trp	Lys	Arg	Pro	Pro	Glu	Asn	Glu	Ala	Pro	Pro	Val	335	340	345
Pro	Phe	Leu	His	Ala	Gln	Arg	Tyr	Val	Ser	Gly	Tyr	Gly	Leu	Gln	350	355	360
Lys	Gly	Glu	Leu	Ser	Thr	Leu	Leu	Tyr	Asn	Thr	His	Pro	Tyr	Arg	365	370	375
Ala	Phe	Pro	Val	Leu	Leu	Leu	Asp	Thr	Val	Pro	Trp	Tyr	Leu	Arg	380	385	390
Leu	Tyr	Val	His	Thr	Leu	Thr	Ile	Thr	Ser	Lys	Gly	Lys	Glu	Asn	395	400	405
Lys	Pro	Ser	Tyr	Ile	His	Tyr	Gln	Pro	Ala	Gln	Asp	Arg	Leu	Gln	410	415	420
Pro	His	Leu	Leu	Glu	Met	Leu	Ile	Gln	Leu	Pro	Ala	Asn	Ser	Val	425	430	435
Thr	Lys	Val	Ser	Ile	Gln	Phe	Glu	Arg	Ala	Leu	Leu	Lys	Trp	Thr	440	445	450
Glu	Tyr	Thr	Pro	Asp	Pro	Asn	His	Gly	Phe	Tyr	Val	Ser	Pro	Ser	455	460	465

Val	Leu	Ser	Ala	Leu	Val	Pro	Ser	Met	Val	Ala	Ala	Lys	Pro	Val	
				470					475					480	
Asp	Trp	Glu	Glu	Ser	Pro	Leu	Phe	Asn	Ser	Leu	Phe	Pro	Val	Ser	
				485					490					495	
Asp	Gly	Ser	Asn	Tyr	Phe	Val	Arg	Leu	Tyr	Thr	Glu	Pro	Leu	Leu	
				500					505					510	
Val	Asn	Leu	Pro	Thr	Pro	Asp	Phe	Ser	Met	Pro	Tyr	Asn	Val	Ile	
				515					520					525	
Cys	Leu	Thr	Cys	Thr	Val	Val	Ala	Val	Cys	Tyr	Gly	Ser	Phe	Tyr	
				530					535					540	
Asn	Leu	Leu	Thr	Arg	Thr	Phe	His	Ile	Glu	Glu	Pro	Arg	Thr	Gly	
				545					550					555	
Gly	Leu	Ala	Lys	Arg	Leu	Ala	Asn	Leu	Ile	Arg	Arg	Ala	Arg	Gly	
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Val Pro Pro Leu

<210> 341  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 341  
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<210> 342  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

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 <221> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe

<400> 342  
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<210> 343  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

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<400> 343  
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<210> 344  
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 <212> DNA  
 <213> Homo sapiens

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 tgaccctggg ggctgtggaa ggagttaaag agggatataga gaaagcaggg 100  
 gtttgccag ctgacaacgt acgtgcttc aagtccgac ctccccagt 150  
 tcacacagac caggactgtc tgggggaaag gaagtgttgt tacctgcact 200  
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 gagacttgga atatggaaga agcaataccc aacccacca aagaaaacct 450  
 gagcttgaag tccttttccc caaaaagagg gaagagtcac aaaaagtcca 500  
 gacccaggg acggtacttt ccctctctac ctggtgtctc tccctaatgc 550  
 tcatgaatgg acccctcatg aatgaaacca gtgcccttat aagagacccc 600  
 aaagagctgc cttgcccttc tgcaatgtgt gatcacagct agaaggcact 650  
 gtcagagaag agaaactggc cctcaccaga tgctgaatct gctgggtgcct 700  
 tgatcttggga cttcccagcc tctagaactg taagaaataa atatttgctg 750  
 tttataatcc aa 762

<210> 345  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 345  
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 Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys  
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 35 40 45  
 Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys  
 50 55 60  
 Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys  
 65 70 75  
 Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro  
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 Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser  
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 Thr Arg Cys Pro Gln Lys  
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<210> 346  
 <211> 2528  
 <212> DNA  
 <213> Homo sapiens

<400> 346  
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 attttctaca gtgaaaaaaaa aaaaaaaaa 2528

<210> 347  
 <211> 600  
 <212> PRT  
 <213> Homo sapiens

<400> 347  
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                   20                  25                  30  
 Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His  
                   35                  40                  45  
 Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala  
                   50                  55                  60  
 Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

65										70					75				
Tyr	Ala	Glu	Pro	Ala	Pro	Glu	Asn	Asn	Ala	Leu	Asn	Thr	Gln	Thr					
				80					85										90
Gln	Pro	Lys	Ala	His	Thr	Thr	Gly	Asp	Arg	Gly	Lys	Glu	Ala	Asn					
				95					100					105					
Gln	Ala	Pro	Pro	Glu	Glu	Gln	Asp	Lys	Val	Pro	His	Thr	Ala	Gln					
				110					115					120					
Arg	Ala	Ala	Trp	Lys	Ser	Pro	Glu	Lys	Glu	Lys	Thr	Met	Val	Asn					
				125					130					135					
Thr	Leu	Ser	Pro	Arg	Gly	Gln	Asp	Ala	Gly	Met	Ala	Ser	Gly	Arg					
				140					145					150					
Thr	Glu	Ala	Gln	Ser	Trp	Lys	Ser	Gln	Asp	Thr	Lys	Thr	Thr	Gln					
				155					160					165					
Gly	Asn	Gly	Gly	Gln	Thr	Arg	Lys	Leu	Thr	Ala	Ser	Arg	Thr	Val					
				170					175					180					
Ser	Glu	Lys	His	Gln	Gly	Lys	Ala	Ala	Thr	Thr	Ala	Lys	Thr	Leu					
				185					190					195					
Ile	Pro	Lys	Ser	Gln	His	Arg	Met	Leu	Ala	Pro	Thr	Gly	Ala	Val					
				200					205					210					
Ser	Thr	Arg	Thr	Arg	Gln	Lys	Gly	Val	Thr	Thr	Ala	Val	Ile	Pro					
				215					220					225					
Pro	Lys	Glu	Lys	Lys	Pro	Gln	Ala	Thr	Pro	Pro	Pro	Ala	Pro	Phe					
				230					235					240					
Gln	Ser	Pro	Thr	Thr	Gln	Arg	Asn	Gln	Arg	Leu	Lys	Ala	Ala	Asn					
				245					250					255					
Phe	Lys	Ser	Glu	Pro	Arg	Trp	Asp	Phe	Glu	Glu	Lys	Tyr	Ser	Phe					
				260					265					270					
Glu	Ile	Gly	Gly	Leu	Gln	Thr	Thr	Cys	Pro	Asp	Ser	Val	Lys	Ile					
				275					280					285					
Lys	Ala	Ser	Lys	Ser	Leu	Trp	Leu	Gln	Lys	Leu	Phe	Leu	Pro	Asn					
				290					295					300					
Leu	Thr	Leu	Phe	Leu	Asp	Ser	Arg	His	Phe	Asn	Gln	Ser	Glu	Trp					
				305					310					315					
Asp	Arg	Leu	Glu	His	Phe	Ala	Pro	Pro	Phe	Gly	Phe	Met	Glu	Leu					
				320					325					330					
Asn	Tyr	Ser	Leu	Val	Gln	Lys	Val	Val	Thr	Arg	Phe	Pro	Pro	Val					
				335					340					345					
Pro	Gln	Gln	Gln	Leu	Leu	Leu	Ala	Ser	Leu	Pro	Ala	Gly	Ser	Leu					
				350					355					360					
Arg	Cys	Ile	Thr	Cys	Ala	Val	Val	Gly	Asn	Gly	Gly	Ile	Leu	Asn					
				365					370					375					
Asn	Ser	His	Met	Gly	Gln	Glu	Ile	Asp	Ser	His	Asp	Tyr	Val	Phe					

380	385	390
Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly		
395	400	405
Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln		
410	415	420
Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn Val Pro Leu		
425	430	435
Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asp		
440	445	450
Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met Ser		
455	460	465
Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg		
470	475	480
Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe		
485	490	495
Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp		
500	505	510
Gly Ala His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu		
515	520	525
Leu Leu Thr Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly		
530	535	540
Phe Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp		
545	550	555
Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Lys		
560	565	570
Leu Glu Arg Glu Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile		
575	580	585
Arg Leu Tyr Gln Arg Pro Gly Pro Gly Thr Ala Lys Ala Lys Asn		
590	595	600

<210> 348

<211> 496

<212> DNA

<213> Homo sapiens

<400> 348

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agtgcagcaa acacttccat agactttatc acaacaccag agactgcacc 200

attcctgcat actataaaag atgcgccagg cttcttacct ggctggctgt 250

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<210> 351

<211> 197

<212> PRT

<213> Homo sapiens

<400> 351

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Cys	Leu	Trp	Tyr	Leu	Asp	Arg	Asn	Gly	Ser	Trp	His	Pro	Gly	Phe	35	40	45	
Asn	Cys	Glu	Phe	Phe	Thr	Phe	Cys	Cys	Gly	Thr	Cys	Tyr	His	Arg	50	55	60	
Tyr	Cys	Cys	Arg	Asp	Leu	Thr	Leu	Leu	Ile	Thr	Glu	Arg	Gln	Gln	65	70	75	
Lys	His	Cys	Leu	Ala	Phe	Ser	Pro	Lys	Thr	Ile	Ala	Gly	Ile	Ala	80	85	90	
Ser	Ala	Val	Ile	Leu	Phe	Val	Ala	Val	Val	Ala	Thr	Thr	Ile	Cys	95	100	105	
Cys	Phe	Leu	Cys	Ser	Cys	Cys	Tyr	Leu	Tyr	Arg	Arg	Arg	Gln	Gln	110	115	120	
Leu	Gln	Ser	Pro	Phe	Glu	Gly	Gln	Glu	Ile	Pro	Met	Thr	Gly	Ile	125	130	135	
Pro	Val	Gln	Pro	Val	Tyr	Pro	Tyr	Pro	Gln	Asp	Pro	Lys	Ala	Gly	140	145	150	
Pro	Ala	Pro	Pro	Gln	Pro	Gly	Phe	Met	Tyr	Pro	Pro	Ser	Gly	Pro	155	160	165	
Ala	Pro	Gln	Tyr	Pro	Leu	Tyr	Pro	Ala	Gly	Pro	Pro	Val	Tyr	Asn	170	175	180	



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Thr	Asp	Val	Leu	Ile	Leu	Pro	Glu	Glu	Val	Glu	Trp	Ile	Lys	Phe
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Gly	Trp	Asp	Ser	Leu	Thr	Gly	Leu	Leu	Lys	Gly	Thr	His	Thr	Ala
				620					625					630
Val	Ser	Ser	Asn	Asp	Arg	Ala	Ser	Leu	Ile	Asn	Asn	Ala	Phe	Gln
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Cys	Val	His	Asn	Tyr	Gln	Pro	Cys	Val	Gln	Arg	Ala	Glu	Gly	Tyr
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Phe	Arg	Lys	Trp	Lys	Glu	Ser	Asn	Gly	Asn	Leu	Ser	Leu	Pro	Val
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Asp	Val	Thr	Leu	Ala	Val	Phe	Ala	Val	Gly	Ala	Gln	Ser	Thr	Glu
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Thr	Glu	Lys	Ser	Gln	Ile	Glu	Phe	Ala	Leu	Cys	Arg	Thr	Gln	Asn
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Lys	Glu	Lys	Leu	Gln	Trp	Leu	Leu	Asp	Glu	Ser	Phe	Lys	Gly	Asp
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Lys	Ile	Lys	Thr	Gln	Glu	Phe	Pro	Gln	Ile	Leu	Thr	Leu	Ile	Gly
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<210> 357  
 <211> 271  
 <212> PRT  
 <213> Homo sapiens

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 Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp  
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 <212> PRT  
 <213> Homo sapiens

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 Val Pro Gly Gly Gly Arg Ser Lys Arg Asp Pro Asp Leu Tyr Gln  
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 65 70 75  
 Ser Pro Glu Lys Arg Asp Met His Asp Phe Phe Val Gly Leu Met  
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 Gly Lys Arg Ser Val Gln Pro Glu Gly Lys Thr Gly Pro Phe Leu  
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<211> 1738  
<212> DNA  
<213> Homo sapiens

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<210> 363  
<211> 78  
<212> PRT  
<213> Homo sapiens

<400> 363  
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Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu  
35 40 45  
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly  
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Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val  
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Cys Asn Thr

<210> 364  
<211> 826  
<212> DNA  
<213> Homo sapiens

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Phe	Phe	His	Asn	Gln	Ala	Thr	Ser	Asn	Glu	Ile	Ile	Lys	Tyr	Asn
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Leu	Gln	Lys	Arg	Thr	Val	Glu	Asp	Arg	Met	Leu	Leu	Pro	Gly	Gly
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Val	Gly	Arg	Ala	Leu	Val	Tyr	Gln	His	Ser	Pro	Ser	Thr	Tyr	Ile
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Asp	Leu	Ala	Val	Asp	Glu	His	Gly	Leu	Trp	Ala	Ile	His	Ser	Gly
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Pro	Gly	Thr	His	Ser	His	Leu	Val	Leu	Thr	Lys	Ile	Glu	Pro	Gly
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Thr	Leu	Gly	Val	Glu	His	Ser	Trp	Asp	Thr	Pro	Cys	Arg	Ser	Gln
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Asp	Ala	Glu	Ala	Ser	Phe	Leu	Leu	Cys	Gly	Val	Leu	Tyr	Val	Val
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Tyr	Ser	Thr	Gly	Gly	Gln	Gly	Pro	His	Arg	Ile	Thr	Cys	Ile	Tyr
				335					340					345
Asp	Pro	Leu	Gly	Thr	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Asn	Leu	Phe
				350					355					360
Phe	Pro	Lys	Arg	Pro	Arg	Ser	His	Ser	Met	Ile	His	Tyr	Asn	Pro
				365					370					375
Arg	Asp	Lys	Gln	Leu	Tyr	Ala	Trp	Asn	Glu	Gly	Asn	Gln	Ile	Ile
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 <211> 2281  
 <212> DNA  
 <213> Homo sapiens

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<210> 369  
<211> 447  
<212> PRT  
<213> Homo sapiens

<400> 369

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Leu	Gly	Leu	Leu	Ala	Leu	Met	Ala	Thr	Ala	Ala	Val	Ala	Arg	Gly	20	25	30	
Trp	Leu	Arg	Ala	Gly	Glu	Glu	Arg	Ser	Gly	Arg	Pro	Ala	Cys	Gln	35	40	45	
Lys	Ala	Asn	Gly	Phe	Pro	Pro	Asp	Lys	Ser	Ser	Gly	Ser	Lys	Lys	50	55	60	
Gln	Lys	Gln	Tyr	Gln	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Gln	Gln	His	65	70	75	
Asn	Phe	Thr	His	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Lys	Ser	His	Ser	80	85	90	
Gly	Asn	Ile	Ser	Cys	Met	Asp	Phe	Ser	Ser	Asn	Gly	Lys	Tyr	Leu	95	100	105	
Ala	Thr	Cys	Ala	Asp	Asp	Arg	Thr	Ile	Arg	Ile	Trp	Ser	Thr	Lys	110	115	120	
Asp	Phe	Leu	Gln	Arg	Glu	His	Arg	Ser	Met	Arg	Ala	Asn	Val	Glu	125	130	135	
Leu	Asp	His	Ala	Thr	Leu	Val	Arg	Phe	Ser	Pro	Asp	Cys	Arg	Ala	140	145	150	
Phe	Ile	Val	Trp	Leu	Ala	Asn	Gly	Asp	Thr	Leu	Arg	Val	Phe	Lys	155	160	165	
Met	Thr	Lys	Arg	Glu	Asp	Gly	Gly	Tyr	Thr	Phe	Thr	Ala	Thr	Pro	170	175	180	
Glu	Asp	Phe	Pro	Lys	Lys	His	Lys	Ala	Pro	Val	Ile	Asp	Ile	Gly	185	190	195	
Ile	Ala	Asn	Thr	Gly	Lys	Phe	Ile	Met	Thr	Ala	Ser	Ser	Asp	Thr	200	205	210	
Thr	Val	Leu	Ile	Trp	Ser	Leu	Lys	Gly	Gln	Val	Leu	Ser	Thr	Ile	215	220	225	
Asn	Thr	Asn	Gln	Met	Asn	Asn	Thr	His	Ala	Ala	Val	Ser	Pro	Cys	230	235	240	

Gly	Arg	Phe	Val	Ala	Ser	Cys	Gly	Phe	Thr	Pro	Asp	Val	Lys	Val	245	250	255
Trp	Glu	Val	Cys	Phe	Gly	Lys	Lys	Gly	Glu	Phe	Gln	Glu	Val	Val	260	265	270
Arg	Ala	Phe	Glu	Leu	Lys	Gly	His	Ser	Ala	Ala	Val	His	Ser	Phe	275	280	285
Ala	Phe	Ser	Asn	Asp	Ser	Arg	Arg	Met	Ala	Ser	Val	Ser	Lys	Asp	290	295	300
Gly	Thr	Trp	Lys	Leu	Trp	Asp	Thr	Asp	Val	Glu	Tyr	Lys	Lys	Lys	305	310	315
Gln	Asp	Pro	Tyr	Leu	Leu	Lys	Thr	Gly	Arg	Phe	Glu	Glu	Ala	Ala	320	325	330
Gly	Ala	Ala	Pro	Cys	Arg	Leu	Ala	Leu	Ser	Pro	Asn	Ala	Gln	Val	335	340	345
Leu	Ala	Leu	Ala	Ser	Gly	Ser	Ser	Ile	His	Leu	Tyr	Asn	Thr	Arg	350	355	360
Arg	Gly	Glu	Lys	Glu	Glu	Cys	Phe	Glu	Arg	Val	His	Gly	Glu	Cys	365	370	375
Ile	Ala	Asn	Leu	Ser	Phe	Asp	Ile	Thr	Gly	Arg	Phe	Leu	Ala	Ser	380	385	390
Cys	Gly	Asp	Arg	Ala	Val	Arg	Leu	Phe	His	Asn	Thr	Pro	Gly	His	395	400	405
Arg	Ala	Met	Val	Glu	Glu	Met	Gln	Gly	His	Leu	Lys	Arg	Ala	Ser	410	415	420
Asn	Glu	Ser	Thr	Arg	Gln	Arg	Leu	Gln	Gln	Gln	Leu	Thr	Gln	Ala	425	430	435
Gln	Glu	Thr	Leu	Lys	Ser	Leu	Gly	Ala	Leu	Lys	Lys				440	445	

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 <212> DNA  
 <213> Homo sapiens

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<210> 371

<211> 105

<212> PRT

<213> Homo sapiens

<400> 371

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				20					25					30
Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg
				35					40					45
Gly	Leu	Arg	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys
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His	Pro	Gly	Ser	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His
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<210> 373  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 373

Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp
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Ser	Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu
				20					25					30
Leu	Ala	Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala
				35					40					45
Leu	Glu	Tyr	Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu
				50					55					60
Pro	Arg	Thr	Phe	Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala
				65					70					75
Val	Ile	Met	Ala	Val	Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu
				80					85					90
Glu	Ala	Ala	Asp	Leu	Ser	Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu
				95					100					105
Gly	Val	Pro	Leu	Tyr	Ala	Val	Val	Lys	Glu	His	Ile	Arg	Thr	Glu
				110					115					120
Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe	Lys	Gly	Glu	Ile	Phe	Leu	Asp
				125					130					135
Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln	Arg	Arg	Lys	Met	Met	Phe
				140					145					150
Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr	Asn	Phe	Phe	Arg	Ala
				155					160					165
Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly	Glu	Gly	Phe	Ile
				170					175					180
Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Lys	Gln	Gly	Ile	Leu
				185					190					195
Leu	Glu	His	Arg	Glu	Lys	Glu	Phe	Gly	Asp	Lys	Val	Asn	Leu	Leu
				200					205					210
Ser	Val	Leu	Glu	Ala	Ala	Lys	Met	Ile	Lys	Pro	Gln	Thr	Leu	Ala
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Ser Glu Lys Lys

<210> 374  
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 <212> DNA  
 <213> Homo sapiens

<400> 374

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<211> 919

<213> Home

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Phe Glu Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp  
35 40 45

Glu Lys Ile Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser  
50 55 60

Thr Tyr Leu Phe Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn  
65 70 75

Val Ser Ile Leu Ile Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr  
80 85 90

Lys Arg Pro Lys His Glu Asn His Lys His Ala Asp Val Ile Val  
95 100 105

Ala Pro Pro Thr Leu Pro Gly Arg Asp Glu Pro Tyr Thr Lys Gln  
110 115 120

Phe Thr Glu Cys Gly Glu Lys Gly Glu Tyr Ile His Phe Thr Pro  
125 130 135

Asp Leu Leu Leu Gly Lys Lys Gln Asn Glu Tyr Gly Pro Pro Gly  
140 145 150

Lys Leu Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe  
155 160 165

Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys  
170 175 180

Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser Gly Arg Asn  
185 190 195

Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg Ala Cys  
200 205 210

Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln Phe  
215 220 225

Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met  
230 235 240

Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His  
245 250 255

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Asn  Gln  Glu  Ala  Pro  Ser  Leu  Gln  Asn  Ile  Lys  Cys  Asn  Phe  Arg
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Ser Thr Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr

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Ile Pro Met Val Thr	Pro Pro Pro Pro	Pro Val Phe Ser Leu	Leu		
	290		295		300
Lys Ile Ser Gln Arg	Ile Val Cys Leu	Val Leu Asp Lys Ser	Gly		
	305		310		315
Ser Met Gly Gly Lys	Asp Arg Leu Asn	Arg Met Asn Gln Ala	Ala		
	320		325		330
Lys His Phe Leu Leu	Gln Thr Val Glu	Asn Gly Ser Trp Val	Gly		
	335		340		345
Met Val His Phe Asp	Ser Thr Ala Thr	Ile Val Asn Lys Leu	Ile		
	350		355		360
Gln Ile Lys Ser Ser	Asp Glu Arg Asn	Thr Leu Met Ala Gly	Leu		
	365		370		375
Pro Thr Tyr Pro Leu	Gly Gly Thr Ser	Ile Cys Ser Gly Ile	Lys		
	380		385		390
Tyr Ala Phe Gln Val	Ile Gly Glu Leu	His Ser Gln Leu Asp	Gly		
	395		400		405
Ser Glu Val Leu Leu	Leu Thr Asp Gly	Glu Asp Asn Thr Ala	Ser		
	410		415		420
Ser Cys Ile Asp Glu	Val Lys Gln Ser	Gly Ala Ile Val His	Phe		
	425		430		435
Ile Ala Leu Gly Arg	Ala Ala Asp Glu	Ala Val Ile Glu Met	Ser		
	440		445		450
Lys Ile Thr Gly Gly	Ser His Phe Tyr	Val Ser Asp Glu Ala	Gln		
	455		460		465
Asn Asn Gly Leu Ile	Asp Ala Phe Gly	Ala Leu Thr Ser Gly	Asn		
	470		475		480
Thr Asp Leu Ser Gln	Lys Ser Leu Gln	Leu Glu Ser Lys Gly	Leu		
	485		490		495
Thr Leu Asn Ser Asn	Ala Trp Met Asn	Asp Thr Val Ile Ile	Asp		
	500		505		510
Ser Thr Val Gly Lys	Asp Thr Phe Phe	Leu Ile Thr Trp Asn	Ser		
	515		520		525
Leu Pro Pro Ser Ile	Ser Leu Trp Asp	Pro Ser Gly Thr Ile	Met		
	530		535		540
Glu Asn Phe Thr Val	Asp Ala Thr Ser	Lys Met Ala Tyr Leu	Ser		
	545		550		555
Ile Pro Gly Thr Ala	Lys Val Gly Thr	Trp Ala Tyr Asn Leu	Gln		
	560		565		570
Ala Lys Ala Asn Pro	Glu Thr Leu Thr	Ile Thr Val Thr Ser	Arg		
	575		580		585
Ala Ala Asn Ser Ser	Val Pro Pro Ile	Thr Val Asn Ala Lys	Met		

590					595					600				
Asn	Lys	Asp	Val	Asn	Ser	Phe	Pro	Ser	Pro	Met	Ile	Val	Tyr	Ala
				605					610					615
Glu	Ile	Leu	Gln	Gly	Tyr	Val	Pro	Val	Leu	Gly	Ala	Asn	Val	Thr
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Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ser	Phe	Lys	Asn	Asp	Gly	Val
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Tyr	Ser	Arg	Tyr	Phe	Thr	Ala	Tyr	Thr	Glu	Asn	Gly	Arg	Tyr	Ser
				665					670					675
Leu	Lys	Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg	Leu	Lys
				680					685					690
Leu	Arg	Pro	Pro	Leu	Asn	Arg	Ala	Ala	Tyr	Ile	Pro	Gly	Trp	Val
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Val	Asn	Gly	Glu	Ile	Glu	Ala	Asn	Pro	Pro	Arg	Pro	Glu	Ile	Asp
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Glu	Asp	Thr	Gln	Thr	Thr	Leu	Glu	Asp	Phe	Ser	Arg	Thr	Ala	Ser
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Gly	Gly	Ala	Phe	Val	Val	Ser	Gln	Val	Pro	Ser	Leu	Pro	Leu	Pro
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Asp	Gln	Tyr	Pro	Pro	Ser	Gln	Ile	Thr	Asp	Leu	Asp	Ala	Thr	Val
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His	Glu	Asp	Lys	Ile	Ile	Leu	Thr	Trp	Thr	Ala	Pro	Gly	Asp	Asn
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Phe	Asp	Val	Gly	Lys	Val	Gln	Arg	Tyr	Ile	Ile	Arg	Ile	Ser	Ala
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Ser	Ile	Leu	Asp	Leu	Arg	Asp	Ser	Phe	Asp	Asp	Ala	Leu	Gln	Val
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Asn	Thr	Thr	Asp	Leu	Ser	Pro	Lys	Glu	Ala	Asn	Ser	Lys	Glu	Ser
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Phe	Ala	Phe	Lys	Pro	Glu	Asn	Ile	Ser	Glu	Glu	Asn	Ala	Thr	His
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Ile	Phe	Ile	Ala	Ile	Lys	Ser	Ile	Asp	Lys	Ser	Asn	Leu	Thr	Ser
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Lys	Val	Ser	Asn	Ile	Ala	Gln	Val	Thr	Leu	Phe	Ile	Pro	Gln	Ala
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Asn	Pro	Asp	Asp	Ile	Asp	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Pro
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Thr	Pro	Asp	Lys	Ser	His	Asn	Ser	Gly	Val	Asn	Ile	Ser	Thr	Leu
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Val	Leu	Ser	Val	Ile	Gly	Ser	Val	Val	Ile	Val	Asn	Phe	Ile	Leu



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 tatocagttc ttttcagtca gtacaatcct ggcataatat acggccacca 1850  
 tgatgcagtc cctcccttgg aacagcagct ggtcataaag aaggaaactg 1900  
 gattttggag agacttttga tttgggatga cgtgtcagta tcggtcagac 1950  
 ttcatcaata taggtgggtt tgatctggac atcaaaggct ggggcggaga 2000  
 ggatgtgcac ctttatcgca agtatctcca cagcaacctc atagtggtag 2050  
 ggacgcctgt gcgaggactc ttccacctct ggcatgagaa gcgctgcatg 2100  
 gacgagctga ccccgagca gtacaagatg tgcatgcagt ccaaggccat 2150  
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 tagaggctca ctttcgcaaa cagaaacaga agacaagtag caaaaaaaca 2250  
 tgaactccca gagaaggatt gtgggagaca ctttttcttt ctttttgcaa 2300  
 ttactgaaag tggtgcacac agagaaaaga cttccataaa ggacgacaaa 2350  
 agaattggac tgatgggtca gagatgagaa agcctccgat ttctctctgt 2400  
 tgggcttttt acaacagaaa tcaaatctc cgctttgcct gcaaaagtaa 2450  
 cccagttgca ccctgtgaag tgtctgacaa aggcagaatg cttgtgagat 2500  
 tataagccta atggtgtgga ggttttgatg gtgtttacaa tacactgaga 2550  
 cctgttggtt tgtgtgctca ttgaaatatt catgatttaa gagcagtttt 2600  
 gtaaaaaatt cattagcatg aaaggcaagc atatttctcc tcatatgaat 2650  
 gagcctatca gcagggtct agtttctagg aatgctaaaa tatcagaagg 2700  
 caggagagga gataggctta ttatgatact agtgagtaca ttaagtaaaa 2750  
 taaaatggac cagaaaagaa aagaaaccat aaatatcgtg tcatattttc 2800  
 cccaagatta accaaaaata atctgcttat ctttttggtt gtccttttaa 2850  
 ctgtctccgt tttttcttt tatttaaaaa tgcacttttt ttcccttgtg 2900



Glu	Gln	Leu	Arg	Asn	Gly	Gln	Tyr	Gln	Ala	Ser	Asp	Ala	Ala	Gly	
				95					100					105	
Leu	Gly	Leu	Asp	Arg	Ser	Pro	Pro	Glu	Lys	Thr	Gln	Ala	Asp	Leu	
				110					115					120	
Leu	Ala	Phe	Leu	His	Ser	Gln	Val	Asp	Lys	Ala	Glu	Val	Asn	Ala	
				125					130					135	
Gly	Val	Lys	Leu	Ala	Thr	Glu	Tyr	Ala	Ala	Val	Pro	Phe	Asp	Ser	
				140					145					150	
Phe	Thr	Leu	Gln	Lys	Val	Tyr	Gln	Leu	Glu	Thr	Gly	Leu	Thr	Arg	
				155					160					165	
His	Pro	Glu	Glu	Lys	Pro	Val	Arg	Lys	Asp	Lys	Arg	Asp	Glu	Leu	
				170					175					180	
Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Thr	Leu	Asn	Asn	Pro	Ala	
				185					190					195	
Glu	Asn	Ser	Pro	Asn	His	Arg	Pro	Tyr	Thr	Ala	Ser	Asp	Phe	Ile	
				200					205					210	
Glu	Gly	Ile	Tyr	Arg	Thr	Glu	Arg	Asp	Lys	Gly	Thr	Leu	Tyr	Glu	
				215					220					225	
Leu	Thr	Phe	Lys	Gly	Asp	His	Lys	His	Glu	Phe	Lys	Arg	Leu	Ile	
				230					235					240	
Leu	Phe	Arg	Pro	Phe	Ser	Pro	Ile	Met	Lys	Val	Lys	Asn	Glu	Lys	
				245					250					255	
Leu	Asn	Met	Ala	Asn	Thr	Leu	Ile	Asn	Val	Ile	Val	Pro	Leu	Ala	
				260					265					270	
Lys	Arg	Val	Asp	Lys	Phe	Arg	Gln	Phe	Met	Gln	Asn	Phe	Arg	Glu	
				275					280					285	
Met	Cys	Ile	Glu	Gln	Asp	Gly	Arg	Val	His	Leu	Thr	Val	Val	Tyr	
				290					295					300	
Phe	Gly	Lys	Glu	Glu	Ile	Asn	Glu	Val	Lys	Gly	Ile	Leu	Glu	Asn	
				305					310					315	
Thr	Ser	Lys	Ala	Ala	Asn	Phe	Arg	Asn	Phe	Thr	Phe	Ile	Gln	Leu	
				320					325					330	
Asn	Gly	Glu	Phe	Ser	Arg	Gly	Lys	Gly	Leu	Asp	Val	Gly	Ala	Arg	
				335					340					345	
Phe	Trp	Lys	Gly	Ser	Asn	Val	Leu	Leu	Phe	Phe	Cys	Asp	Val	Asp	
				350					355					360	
Ile	Tyr	Phe	Thr	Ser	Glu	Phe	Leu	Asn	Thr	Cys	Arg	Leu	Asn	Thr	
				365					370					375	
Gln	Pro	Gly	Lys	Lys	Val	Phe	Tyr	Pro	Val	Leu	Phe	Ser	Gln	Tyr	
				380					385					390	
Asn	Pro	Gly	Ile	Ile	Tyr	Gly	His	His	Asp	Ala	Val	Pro	Pro	Leu	
				395					400					405	



Glu	Gln	Gln	Leu	Val	Ile	Lys	Lys	Glu	Thr	Gly	Phe	Trp	Arg	Asp	
				410					415					420	
Phe	Gly	Phe	Gly	Met	Thr	Cys	Gln	Tyr	Arg	Ser	Asp	Phe	Ile	Asn	
				425					430					435	
Ile	Gly	Gly	Phe	Asp	Leu	Asp	Ile	Lys	Gly	Trp	Gly	Gly	Glu	Asp	
				440					445					450	
Val	His	Leu	Tyr	Arg	Lys	Tyr	Leu	His	Ser	Asn	Leu	Ile	Val	Val	
				455					460					465	
Arg	Thr	Pro	Val	Arg	Gly	Leu	Phe	His	Leu	Trp	His	Glu	Lys	Arg	
				470					475					480	
Cys	Met	Asp	Glu	Leu	Thr	Pro	Glu	Gln	Tyr	Lys	Met	Cys	Met	Gln	
				485					490					495	
Ser	Lys	Ala	Met	Asn	Glu	Ala	Ser	His	Gly	Gln	Leu	Gly	Met	Leu	
				500					505					510	
Val	Phe	Arg	His	Glu	Ile	Glu	Ala	His	Leu	Arg	Lys	Gln	Lys	Gln	
				515					520					525	
Lys	Thr	Ser	Ser	Lys	Lys	Thr									
				530											

<210> 382

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

ctcggggaaa gggacttgat gttgg 25

<210> 383

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gcgaaggtga gcctctatct cgtgcc 26

<210> 384

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 384

cagcctacac gtattgagg 19

<210> 385

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

cagtcagtac aatcctggca taatatacgg ccaccatgat gcagtcctc 48

<210> 386

<211> 1346

<212> DNA

<213> Homo sapiens

<400> 386

gaaagaatgt tgtggctgct cttttttctg gtgactgccca ttcattgctga 50  
actctgtcaa ccagggtgcag aaaatgcttt taaagtgaga cttagtatca 100  
gaacagctct gggagataaa gcatatgcct gggataccaa tgaagaatac 150  
ctcttcaaag cgatggtagc tttctccatg agaaaagttc ccaacagaga 200  
agcaacagaa atttcccatg tctactttg caatgtaacc cagagggtat 250  
cattctgggt tgtgggttaca gacccttcaa aaaatcacac ctttctgct 300  
gttgagggtgc aatcagccat aagaatgaac aagaaccgga tcaacaatgc 350  
cttctttcta aatgaccaa ctctggaatt tttaaaaatc ctttccacac 400  
ttgcaccacc catggaccca tctgtgccc tctggattat tatatttgg 450  
gtgatatttt gcatcatcat agttgcaatt gcactactga ttttatcagg 500  
gatctggcaa cgtagaagaa agaacaaaga accatctgaa gtggatgacg 550  
ctgaagataa gtgtgaaaac atgatcacia ttgaaaatgg catccccctc 600  
gatccccctg acatgaaggg gggcatatta atgatgcctt catgacagag 650  
gatgagaggc tcaccctct ctgaagggt gttgttctgc ttcctcaaga 700  
aattaaacat ttgtttctgt gtgactgctg agcatcctga aataccaaga 750  
gcagatcata tattttgttt caccattctt cttttgtaat aaattttgaa 800  
tgtgcttgaa agtgaaaagc aatcaattat accaccaac accactgaaa 850  
tcataagcta ttcacgactc aaaatattct aaaatatttt tctgacagta 900  
tagtgtataa atgtggctcat gtggtatttg tagttattga ttttagcatt 950  
tttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct 1000  
aaggaaaaat aaattttcca gtggagaata catataatat ggtgtagaaa 1050  
tcattgaaaa tggatccttt ttgacgatca cttatatcac tctgtatatg 1100  
actaagtaaa caaaagtga aagtaattat tgtaaatgga tggataaaaa 1150  
tggaattact catatacagg gtggaatttt atcctgttat cacaccaaca 1200  
gttgattata tattttctga atatcagccc ctaataggac aattctattt 1250

gttgaccatt tctacaattt gtaaaagtcc aatctgtgct aacttaataa 1300

agtaataatc atctctttttt aaaaaaaaaa aaaaaaaaaa aaaaaa 1346

<210> 387

<211> 212

<212> PRT

<213> Homo sapiens

<400> 387

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu  
1 5 10 15

Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser  
20 25 30

Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn  
35 40 45

Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys  
50 55 60

Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys  
65 70 75

Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp Pro  
80 85 90

Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile  
95 100 105

Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp  
110 115 120

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro  
125 130 135

Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile  
140 145 150

Phe Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly  
155 160 165

Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp  
170 175 180

Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile Glu Asn Gly  
185 190 195

Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly Ile Leu Met Met  
200 205 210

Pro Ser

<210> 388

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 388

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gccaaggctg ggtttccctc atgtatggca agagctctac tcgtgcgggtg 150  
cttcttctcc ttggcataca gctcacagct ctttggccta tagcagctgt 200  
ggaaatttat acctcccggg tgctggaggc tgtaaatggg acagatgctc 250  
ggttaaaatg cactttctcc agctttgccc ctgtgggtga tgctctaaca 300  
gtgacctgga attttctgccc tctagacggg ggacctgagc agtttgtatt 350  
ctactaccac atagatccct tccaacccat gagtgggagg ttttaaggacc 400  
gggtgtcttg ggatgggaat cctgagcggg acgatgcctc catccttctc 450  
tggaactgac agttcgacga caatgggaca tacacctgcc aggtgaagaa 500  
cccacctgat gttgatgggg tgatagggga gatccggctc agcgtcgtgc 550  
aactgtacg cttctctgag atccacttcc tggctctggc cattggctct 600  
gcctgtgcac tgatgatcat aatagtaatt gtagtgggtc tcttccagca 650  
ttaccggaaa aagcgatggg ccgaaagagc tcataaagtg gtggagataa 700  
aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggc ctctgtttat 750  
ttagaagaca cagactaaca attttagatg gaagctgaga tgatttccaa 800  
gaacaagaac cctagtattt cttgaagtta atggaaactt ttctttggct 850  
tttccagttg tgaccggtt tccaaccagt tctgcagcat attagattct 900  
agacaagcaa caccctctg gagccagcac agtgctcctc catatcacca 950  
gtcatacaca gctcattat taaggtctta ttttaattca gagtgtaaat 1000  
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ttaagacact acttacagtg ttatgacttg tatacacata tattgggtatc 1100  
aaaggggata aaagccaatt tgtctgttac atttcctttc acgtatttct 1150  
tttagcagca cttctgctac taaagttaat gtgtttactc tctttccttc 1200  
ccacattctc aattaaaagg tgagctaagc ctctcggtg tttctgatta 1250  
acagtaaata ctaaattcaa actgttaaat gacattttta tttttatgtc 1300  
tctccttaac tatgagacac atcttgtttt actgaatttc tttcaatatt 1350  
ccaggtgata gatttttctc g 1371

<210> 389

<211> 215

<212> PRT

<213> Homo sapiens

<400> 389

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Ile	Gln	Leu	Thr	Ala	Leu	Trp	Pro	Ile	Ala	Ala	Val	Glu	Ile	Tyr	
				20					25					30	
Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	
				35					40					45	
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	
				50					55					60	
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	
				65					70					75	
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	
				80					85					90	
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	
				95					100					105	
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	
				110					115					120	
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	
				125					130					135	
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	
				140					145					150	
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	
				155					160					165	
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	
				170					175					180	
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	
				185					190					195	
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	
				200					205					210	
Leu	Glu	Asp	Thr	Asp											
				215											

<210> 390  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 390  
 ccgaggccat ctagaggcca gagc 24

<210> 391  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
 acaggcagag ccaatggcca gagc 24

<210> 392  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 392  
 gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcatg 45

<210> 393  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 393  
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 agcagtcctg gtactcttgg gagtttccat cttttctggc tctgcccaga 100  
 atccgacaac agctgctcca gctgacacgt atccagctac tggtcctgct 150  
 gatgatgaag cccctgatgc tgaaaccact gctgctgcaa ccactgcgac 200  
 cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250  
 aagacattcc agttttaccc aaatggggtg gggatctccc gaatggtaga 300  
 gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350  
 tattcatgct tcctgtgatt tcatccaact acttaccttg cctacgatat 400  
 cccctttatc tctaatacgt ttattttctt tcaaataaaa aataactatg 450  
 agcaacataa aaaaaaaaaa a 471

<210> 394  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 394  
 Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe  
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 Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr  
                     20                    25                    30  
 Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu  
                     35                    40                    45  
 Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr  
                     50                    55                    60  
 Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val  
                     65                    70                    75  
 Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro  
                     80                    85                    90

<210> 395  
 <211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 395  
gctccctgat cttcatgtca ccacc 25

<210> 396  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 396  
cagggacaca ctctaccatt cgaggag 26

<210> 397  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 397  
ccatctttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 398  
ggactctgaa ggtcccaagc agctgctgag gcccccaagg aagtgggtcc 50  
aaccttggac ccctaggggt ctggatttgc tggttaacaa gataacctga 100  
gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150  
gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200  
ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250  
ttggcaaggt ccagcgatgg tccggagtcc acacacagac tggcggcagg 300  
gcaggagggg gacagttctg ttgtgcttgg ttggacagta agagggtctt 350  
ggccagtcca ggggtggggg cggcaaaactc cataaagaac cagaggggtct 400  
gggccccggc cacagagtca tctgcccagc tcctctgctg ctggccagtg 450  
ggagtggcac gaggtggggc tttgtgccag taaaaccaca ggctggattt 500  
gcctgcgggc catggtccct gtctagggca gcaattctca accttcttgc 550  
tctcaggacc ccaaagagct ttcattgtat ctattgattt ttaccacatt 600  
agcaattaaa actgagaaat gggccgggca cgggtggctca cgcctgtaat 650

cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700  
 caagaccagc ctggccaaca tggtgaaacc ttgtctacta aaaatacaaa 750  
 aaattagcca ggcacagtgg tgtgcactgg tagtcccagt tactcggggag 800  
 gctgaggcag gaaaatcgct tgaacccagg aggcggacgt tgcggtgagc 850  
 cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900  
 tcacaca 907

<210> 399  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 399  
 Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala  
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 Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu  
 20 25 30  
 Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly  
 35 40 45  
 Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg  
 50 55 60  
 Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg  
 65 70 75  
 Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn  
 80 85 90  
 Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu  
 95 100 105  
 Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln  
 110 115 120

<210> 400  
 <211> 893  
 <212> DNA  
 <213> Homo sapiens

<400> 400  
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 ccggcctgcc tcagcggccc ccatgggcgg ccagaaactg gcacagcatg 100  
 aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150  
 aacggtgtgt acaggaccac ggagggacgg ctgacaaagg ccaggaacag 200  
 cctgggtctc tatggccgca caatagaact cctggggcag gaggtcagcc 250  
 ggggccggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300  
 atggaggagg atattctgca gctgcaggca gaggccacag ctgaggtgct 350  
 gggggaggtg gccaggcac agaaggtgct acgggacagc gtgcagcggc 400



tagaagtcca gctgaggagc gcctggctgg gccctgccta ccgagaattt 450  
 gaggtcttaa aggctcacgc tgacaagcag agccacatcc tatgggccct 500  
 cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550  
 ggctgcgaca gatccaggag agactccaca cagcggcgct cccagcctga 600  
 atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650  
 cgccccgtga ggccccgtg cagggaggag ctgcctgttc actgggatca 700  
 gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750  
 cggggacaaa ggcagaggat gtagcccat tggggagggg tggaggaagg 800  
 acatgtaccc ttctatgcct acacaccct cattaaagca gagtcgtggc 850  
 atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<400> 401  
 Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala Leu Ala Met Val  
 1 5 10 15  
 Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala  
 20 25 30  
 Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu  
 35 40 45  
 Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu  
 50 55 60  
 Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu  
 65 70 75  
 Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu  
 80 85 90  
 Leu Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu  
 95 100 105  
 Gln Leu Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala  
 110 115 120  
 Gln Ala Gln Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val  
 125 130 135  
 Gln Leu Arg Ser Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu  
 140 145 150  
 Val Leu Lys Ala His Ala Asp Lys Gln Ser His Ile Leu Trp Ala  
 155 160 165  
 Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu Met Val Ala Gln  
 170 175 180  
 Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His Thr Ala Ala

Leu Pro Ala

<210> 402  
 <211> 1915  
 <212> DNA  
 <213> Homo sapiens

<400> 402

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 acacatccag attaaaagcc aggaagcaca gcaaacgtcg agtgagagac 150  
 aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200  
 tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250  
 aagttcacia gaaatgctac cttgcttcag aaggtttgaa gcatttccat 300  
 gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350  
 gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400  
 cagggtgtcaa tgacttttgg ctgggcatca atgacatggt cacggaaggc 450  
 aagtttggtg acgtcaacgg aatcgctatc tccttcctca actgggaccg 500  
 tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550  
 cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatac 600  
 atatgcgagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650  
 agcaagattc atcataactt ataggttcat gatctctaag atcaagtaaa 700  
 aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750  
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 gataaaatgg cttctgctaa acagactaaa atctttctct ctagtctttc 900  
 tcacttgtag aaaccagtt tgttttcaaa aaatcacagt agcaatgcaa 950  
 ctcatcactc tagaaaagca agcttaggct acctgaaaga tttcccttg 1000  
 gaagtttagc gtatgtttga ctaacaaaaa ttccctacat cagagactct 1050  
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 atctcctggt gggacttgta tcttgctctg catatcagaa caciaacccc 1200  
 tgaagagggt ctgatttgat tttttttttt tcttcatgcc tacccttttt 1250  
 ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatattg 1300

atcaattttc attcccacca ttgcattaca acctctaact taaatgggta 1350  
 accctaaggc atatcaaaga agcagattgc atgataaacg gaaatagaaa 1400  
 aaaagaacct acattttattt tgcttttagca tccttactct caccttttat 1450  
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 cttcaaataa atagtgttta aacattgaat gtgttttgtg aacaatatcc 1800  
 cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850  
 tcattgctca ataataaagc ctgaattctg atcaataaaa aaaaaaaaaa 1900  
 aaaaaaaaaa aaaaa 1915

<210> 403  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 403  
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 Ser His Thr Ser Arg Leu Lys Ala Arg Lys His Ser Lys Arg Arg  
 35 40 45  
 Val Arg Asp Lys Asp Gly Asp Leu Lys Thr Gln Ile Glu Lys Leu  
 50 55 60  
 Trp Thr Glu Val Asn Ala Leu Lys Glu Ile Gln Ala Leu Gln Thr  
 65 70 75  
 Val Cys Leu Arg Gly Thr Lys Val His Lys Lys Cys Tyr Leu Ala  
 80 85 90  
 Ser Glu Gly Leu Lys His Phe His Glu Ala Asn Glu Asp Cys Ile  
 95 100 105  
 Ser Lys Gly Gly Ile Leu Val Ile Pro Arg Asn Ser Asp Glu Ile  
 110 115 120  
 Asn Ala Leu Gln Asp Tyr Gly Lys Arg Ser Leu Pro Gly Val Asn  
 125 130 135  
 Asp Phe Trp Leu Gly Ile Asn Asp Met Val Thr Glu Gly Lys Phe  
 140 145 150  
 Val Asp Val Asn Gly Ile Ala Ile Ser Phe Leu Asn Trp Asp Arg

	155		160		165
Ala Gln Pro Asn Gly Gly Lys Arg Glu Asn Cys Val Leu Phe Ser					
	170		175		180
Gln Ser Ala Gln Gly Lys Trp Ser Asp Glu Ala Cys Arg Ser Ser					
	185		190		195
Lys Arg Tyr Ile Cys Glu Phe Thr Ile Pro Lys					
	200		205		

<210> 404  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 404  
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<210> 405  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 405  
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<210> 406  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 406  
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<210> 407  
 <211> 570  
 <212> DNA  
 <213> Homo sapiens

<400> 407  
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 ggctctgcgt ggccctgtcc tgcagctccg ctgctgcttt cttagtgggc 150  
 tcggccaagc ctgtggccca gcctgtcgct gcgctggagt cggcggcgga 200  
 ggccgggggcc gggaccctgg ccaacccctc cggcaccctc aaccgctga 250  
 agctcctgct gagcagcctg ggcatccccg tgaaccacct catagagggc 300  
 tcccagaagt gtgtggctga gctgggtccc caggccgtgg gggccgtgaa 350

ggccctgaag gccctgctgg gggccctgac agtgtttggc tgagccgaga 400  
 ctggagcatc tacacctgag gacaagacgc tgcccacccg cgagggctga 450  
 aaaccccgcc gcggggagga ccgtccatcc ccttcccccg gcccctctca 500  
 ataaacgtgg ttaagagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 550  
 aaaaaaaaaa aaaaaaaaaa 570

<210> 408  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 408

Met	Lys	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Cys	Val	Ala	Leu	Ser	Cys	1	5	10	15
Ser	Ser	Ala	Ala	Ala	Phe	Leu	Val	Gly	Ser	Ala	Lys	Pro	Val	Ala	20	25	30	
Gln	Pro	Val	Ala	Ala	Leu	Glu	Ser	Ala	Ala	Glu	Ala	Gly	Ala	Gly	35	40	45	
Thr	Leu	Ala	Asn	Pro	Leu	Gly	Thr	Leu	Asn	Pro	Leu	Lys	Leu	Leu	50	55	60	
Leu	Ser	Ser	Leu	Gly	Ile	Pro	Val	Asn	His	Leu	Ile	Glu	Gly	Ser	65	70	75	
Gln	Lys	Cys	Val	Ala	Glu	Leu	Gly	Pro	Gln	Ala	Val	Gly	Ala	Val	80	85	90	
Lys	Ala	Leu	Lys	Ala	Leu	Leu	Gly	Ala	Leu	Thr	Val	Phe	Gly	95	100			

<210> 409  
 <211> 2089  
 <212> DNA  
 <213> Homo sapiens

<400> 409

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 ggccccagct cctcagtcgc cagagacccc agcccctcag aaccagacca 200  
 gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250  
 agcgaggaga aggcgggtga ggaagagaaa gcctggctga tggccagcag 300  
 gcagcagctt gccaaggaga cttcaaaactt cggattcagc ctgctgcgaa 350  
 agatctccat gaggcacgat ggcaacatgg tcttctctcc atttggcatg 400  
 tccttgGCCa tgacaggctt gatgctgggg gccacagggc cgactgaaac 450  
 ccagatcaag agagggtcc acttgcaggc cctgaagccc accaagccc 500

ggctcctgcc ttccctcttt aagggaactca gagagaccct ctcccgcac 550  
 ctggaactgg gcctctcaca ggggagtttt gccttcatcc acaaggattt 600  
 tgatgtcaaa gagactttct tcaatttatc caagaggtat ttgatacag 650  
 agtgcgtagc tatgaatttt cgcaatgcct cacaggccaa aaggctcatg 700  
 aatcattaca ttaacaaaga gactcggggg aaaattocca aactgtttga 750  
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 aagggaatg gttgaccca tttgacctg tcttcacga agtcgacact 850  
 ttccacctgg acaagtacaa gaccattaag gtgcccata tgtacggtag 900  
 aggcaagttt gcctccacct ttgacaagaa ttttcgttgt catgtcctca 950  
 aactgcccta ccaaggaaat gccaccatgc tggtagtctt catggagaaa 1000  
 atgggtgacc acctcgccct tgaagactac ctgaccacag acttggtgga 1050  
 gacatggctc agaaacatga aaaccagaaa catggaagtt ttctttccga 1100  
 agttcaagct agatcagaag tatgagatgc atgagctgct taggcagatg 1150  
 ggaatcagaa gaatcttctc accctttgct gaccttagtg aactctcagc 1200  
 tactggaaga aatctccaag tatccagggt ttacgaaga acagtgattg 1250  
 aagttgatga aaggggcaact gaggcagtgg caggaatctt gtcagaaatt 1300  
 actgcttatt ccatgcctcc tgtcatcaaa gtggaccggc catttcattt 1350  
 catgatctat gaagaaacct ctggaatgct tctgtttctg ggcagggtgg 1400  
 tgaatccgac tctcctataa ttcaggacat gcataagcac ttogtgctgt 1450  
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 atggcagggg agagtgttcc tttgttctt aactagttaa ggggtgttctc 1550  
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 cccagcagat gcctgaaacg gtggacagtg ctgaacctta tatatatttt 1650  
 ttctacaca tacataccta tgataaagtt taatttataa attaggcaca 1700  
 gtaagagatt aacaataata acaacattaa gtaaaatgag ttacttgaac 1750  
 gcaagcactg caataccata acagtcaaac tgattataga gaaggctact 1800  
 aagtgactca tgggagagga gcatagacag tgtggagaca ttgggcaagg 1850  
 ggagaattca catcctgggt gggacagagc aggacgatgc aagattccat 1900  
 cccactactc agaatggcat gctgcttaag acttttagat tgtttatttc 1950  
 tggaattttt catttaatgt ttttgacca tggttgacca tggttaactg 2000  
 agactgcaga aagcaaaacc atggataagg gaggactact acaaaagcat 2050  
 taaattgata catatttttt aaaaaaaaaa aaaaaaaaaa 2089

[illegible]

Met	Lys	Val	Val	Pro	Ser	Leu	Leu	Leu	Ser	Val	Leu	Leu	Ala	Gln
1				5					10					15
Val	Trp	Leu	Val	Pro	Gly	Leu	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Glu
				20					25					30
Thr	Pro	Ala	Pro	Gln	Asn	Gln	Thr	Ser	Arg	Val	Val	Gln	Ala	Pro
				35					40					45
Arg	Glu	Glu	Glu	Glu	Asp	Glu	Gln	Glu	Ala	Ser	Glu	Glu	Lys	Ala
				50					55					60
Gly	Glu	Glu	Glu	Lys	Ala	Trp	Leu	Met	Ala	Ser	Arg	Gln	Gln	Leu
				65					70					75
Ala	Lys	Glu	Thr	Ser	Asn	Phe	Gly	Phe	Ser	Leu	Leu	Arg	Lys	Ile
				80					85					90
Ser	Met	Arg	His	Asp	Gly	Asn	Met	Val	Phe	Ser	Pro	Phe	Gly	Met
				95					100					105
Ser	Leu	Ala	Met	Thr	Gly	Leu	Met	Leu	Gly	Ala	Thr	Gly	Pro	Thr
				110					115					120
Glu	Thr	Gln	Ile	Lys	Arg	Gly	Leu	His	Leu	Gln	Ala	Leu	Lys	Pro
				125					130					135
Thr	Lys	Pro	Gly	Leu	Leu	Pro	Ser	Leu	Phe	Lys	Gly	Leu	Arg	Glu
				140					145					150
Thr	Leu	Ser	Arg	Asn	Leu	Glu	Leu	Gly	Leu	Ser	Gln	Gly	Ser	Phe
				155					160					165
Ala	Phe	Ile	His	Lys	Asp	Phe	Asp	Val	Lys	Glu	Thr	Phe	Phe	Asn
				170					175					180
Leu	Ser	Lys	Arg	Tyr	Phe	Asp	Thr	Glu	Cys	Val	Pro	Met	Asn	Phe
				185					190					195
Arg	Asn	Ala	Ser	Gln	Ala	Lys	Arg	Leu	Met	Asn	His	Tyr	Ile	Asn
				200					205					210
Lys	Glu	Thr	Arg	Gly	Lys	Ile	Pro	Lys	Leu	Phe	Asp	Glu	Ile	Asn
				215					220					225
Pro	Glu	Thr	Lys	Leu	Ile	Leu	Val	Asp	Tyr	Ile	Leu	Phe	Lys	Gly
				230					235					240
Lys	Trp	Leu	Thr	Pro	Phe	Asp	Pro	Val	Phe	Thr	Glu	Val	Asp	Thr
				245					250					255
Phe	His	Leu	Asp	Lys	Tyr	Lys	Thr	Ile	Lys	Val	Pro	Met	Met	Tyr
				260					265					270
Gly	Ala	Gly	Lys	Phe	Ala	Ser	Thr	Phe	Asp	Lys	Asn	Phe	Arg	Cys
				275					280					285

His	Val	Leu	Lys	Leu	Pro	Tyr	Gln	Gly	Asn	Ala	Thr	Met	Leu	Val	290	295	300
Val	Leu	Met	Glu	Lys	Met	Gly	Asp	His	Leu	Ala	Leu	Glu	Asp	Tyr	305	310	315
Leu	Thr	Thr	Asp	Leu	Val	Glu	Thr	Trp	Leu	Arg	Asn	Met	Lys	Thr	320	325	330
Arg	Asn	Met	Glu	Val	Phe	Phe	Pro	Lys	Phe	Lys	Leu	Asp	Gln	Lys	335	340	345
Tyr	Glu	Met	His	Glu	Leu	Leu	Arg	Gln	Met	Gly	Ile	Arg	Arg	Ile	350	355	360
Phe	Ser	Pro	Phe	Ala	Asp	Leu	Ser	Glu	Leu	Ser	Ala	Thr	Gly	Arg	365	370	375
Asn	Leu	Gln	Val	Ser	Arg	Val	Leu	Arg	Arg	Thr	Val	Ile	Glu	Val	380	385	390
Asp	Glu	Arg	Gly	Thr	Glu	Ala	Val	Ala	Gly	Ile	Leu	Ser	Glu	Ile	395	400	405
Thr	Ala	Tyr	Ser	Met	Pro	Pro	Val	Ile	Lys	Val	Asp	Arg	Pro	Phe	410	415	420
His	Phe	Met	Ile	Tyr	Glu	Glu	Thr	Ser	Gly	Met	Leu	Leu	Phe	Leu	425	430	435
Gly	Arg	Val	Val	Asn	Pro	Thr	Leu	Leu							440		

<210> 411  
 <211> 636  
 <212> DNA  
 <213> Homo sapiens

<400> 411  
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 gtcaaactact ggccctcaga gcaggaccca gagaaggcct ggggcgcccg 200  
 tgtggtggag cctccggaga aggacgacca gctggtggtg ctgttccctg 250  
 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300  
 aggggcccga tccttccagg caccaaggcc tggatggaga ccgaggacac 350  
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 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450  
 ccaaatacacc aggtgctcct gggaccggag gaagaccaag accacatcta 500  
 ccacccccag tagggctcca ggggccatca ctgccccgc cctgtcccaa 550  
 ggcccagggt gttgggactg ggaccctccc taccctgccc cagctagaca 600



aataaacccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412  
<211> 151  
<212> PRT  
<213> Homo sapiens

<400> 412  
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu  
1 5 10 15  
Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met  
20 25 30  
Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp  
35 40 45  
Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val  
50 55 60  
Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu  
65 70 75  
Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys  
80 85 90  
Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro  
95 100 105  
Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp  
110 115 120  
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln  
125 130 135  
Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro  
140 145 150  
Gln

<210> 413  
<211> 1176  
<212> DNA  
<213> Homo sapiens

<400> 413  
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aggagctctc tgtaccaag gaaagtgcag ctgagactca gacaagatta 100  
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150  
tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200  
gtctccatct ctgccagaa gctgcaagga aatcaaagac gaatgtccta 250  
gtgcatttga tggcctgtat tttctccgca ctgagaatgg tggtatctac 300  
cagaccttct gtgacatgac ctctgggggt ggcggctgga cctggtggc 350  
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450  
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 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550  
 ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600  
 ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650  
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 gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct 850  
 tgtgtgctgg aatgaggggtc accggatgta aactgagca tcaactgcatt 900  
 ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt 950  
 ttctggtttt gattggagtg gatatggaac tcatgttggg tacagcagca 1000  
 gcogtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050  
 tgtgggaggg aaccagacc tctcctcca accatgagat cccaaggatg 1100  
 gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150  
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

<400> 414  
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 Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr  
 20 25 30  
 Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys  
 35 40 45  
 Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr  
 50 55 60  
 Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly  
 65 70 75  
 Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met  
 80 85 90  
 Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly  
 95 100 105  
 Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr  
 110 115 120  
 Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys



ccacaatagt tcagtgcacat ctgctgcttc atcagtaaca atcacaacaa 550  
ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600  
gttggtggta ttgtattaac gctgggagtt ttatctattc tttacattgg 650  
atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700  
aacatgatgc catcatttaa ggaaatccat ggaccaagga tggaatacag 750  
attgatgctg ccctatcaat taattttggt ttattaatag tttaaaacaa 800  
tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850  
gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttggtttt 900  
tgaaataaac atctggatct tatagaccgt tcatacaatg gtttttagcaa 950  
gttcatagta agacaaacaa gtcctatctt ttttttttgg ctggggtggg 1000  
ggcattggtc acatatgacc agtaattgaa agacgcatc actgaaagac 1050  
agaatgccat ctgggcatac aaataagaag tttgtcacag cactcaggat 1100  
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tggatatatc ttaattacta atgccacaca gaaattatac aatcaaacta 1200  
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tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416  
<211> 208  
<212> PRT  
<213> Homo sapiens

<400> 416  
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Thr Leu Gln Val Leu Ala Leu Leu Gly Ala Ala His Glu Ser Ala  
20 25 30  
Ala Met Ala Ala Ser Ala Asn Ile Glu Asn Ser Gly Leu Pro His  
35 40 45  
Asn Ser Ser Ala Asn Ser Thr Glu Thr Leu Gln His Val Pro Ser  
50 55 60  
Asp His Thr Asn Glu Thr Ser Asn Ser Thr Val Lys Pro Pro Thr  
65 70 75  
Ser Val Ala Ser Asp Ser Ser Asn Thr Thr Val Thr Thr Met Lys  
80 85 90  
Pro Thr Ala Ala Ser Asn Thr Thr Thr Pro Gly Met Val Ser Thr  
95 100 105  
Asn Met Thr Ser Thr Thr Leu Lys Ser Thr Pro Lys Thr Thr Ser  
110 115 120  
Val Ser Gln Asn Thr Ser Gln Ile Ser Thr Ser Thr Met Thr Val

	125		130		135
Thr His Asn Ser	Ser Val Thr Ser Ala	Ala Ser Ser Val Thr	Ile		
	140	145	150		
Thr Thr Thr Met	His Ser Glu Ala Lys	Lys Gly Ser Lys Phe	Asp		
	155	160	165		
Thr Gly Ser Phe	Val Gly Gly Ile Val	Leu Thr Leu Gly Val	Leu		
	170	175	180		
Ser Ile Leu Tyr	Ile Gly Cys Lys Met	Tyr Tyr Ser Arg Arg	Gly		
	185	190	195		
Ile Arg Tyr Arg	Thr Ile Asp Glu His	Asp Ala Ile Ile			
	200	205			

<210> 417  
 <211> 1728  
 <212> DNA  
 <213> Homo sapiens

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 gcgatggcga ccctgtgggg aggccttctt cggcttggct ccttgctcag 150  
 cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgag ctgtcagacg 200  
 ccgccaagaa tttcgaggat gtcagatgta aatgtatctg cctccctat 250  
 aaagaaaatt ctgggcatat ttataataag aacatatctc agaaagattg 300  
 tgattgcctt catgtttgtg agcccatgcc tgtgcggggg cctgatgtag 350  
 aagcatactg tctacgctgt gaatgcaa atgaagaaag aagctctgtc 400  
 acaatcaagg ttaccattat aatttatctc tccatttttg gccttctact 450  
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 caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650  
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 tgactgtatt atctgggtat ctgctgtgtc tgcacttcat ggtaaacggg 1300  
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 atttttattt aaacccaagc ctccctggat tgataatata tacacatttg 1550  
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 cagctttgaa ctagggctgg ggttggtggg gcctcttctg aaagggtctaa 1650  
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 <212> PRT  
 <213> Homo sapiens

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 Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile  
 35 40 45  
 Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn  
 50 55 60  
 Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met  
 65 70 75  
 Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu  
 80 85 90  
 Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile  
 95 100 105  
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val  
 110 115 120  
 Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly  
 125 130 135

His	Ala	Gln	Leu	Ile	Gln	Ser	Asp	Asp	Asp	Ile	Gly	Asp	His	Gln
				140					145					150
Pro	Phe	Ala	Asn	Ala	His	Asp	Val	Leu	Ala	Arg	Ser	Arg	Ser	Arg
				155					160					165
Ala	Asn	Val	Leu	Asn	Lys	Val	Glu	Tyr	Ala	Gln	Gln	Arg	Trp	Lys
				170					175					180
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Ser	Val	Phe	Asp	Arg	His	Val
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Val Leu Ser														

<210> 419  
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 <213> Homo sapiens

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 gccttctgt cccgcgggaa gcggcaggag ccgcccga cacctgaagg 150  
 aaaattgggc cgatttccac ctatgatgca tcatcaccag gcacctcag 200  
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 aacttcttat agttcataaa attatttcaa atccatcatc tctttaaatc 500  
 ctgcctctc ttcatgaggt acttaggata gccattattt cagtttcaca 550  
 taagaatgtt tactcaatgt ttaagtgttt tgccccaaaa ttcacaacta 600  
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 gagtataca attcaatgca ctcccctgcc a 681

<210> 420  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

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 Gly Lys Arg Gln Glu Pro Pro Pro Thr Pro Glu Gly Lys Leu Gly  
 35 40 45

Arg Phe Pro Pro Met Met His His His Gln Ala Pro Ser Asp Gly  
50 55 60

Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala  
65 70 75

Phe Ala Lys Ala Lys Gly Ser Gly Gly Gly Ala Gly Gly Gly Gly  
80 85 90

Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe  
95 100 105

Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg  
110 115 120

Ile Ile Leu Ile Ile Leu His Gln  
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<210> 421  
<211> 1630  
<212> DNA  
<213> Homo sapiens

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aactcattcct gctgccagtg ttactggatt attccttggg cctgaatgac 150  
ttgaatgttt cccgcctga gctaacagtc catgtgggtg attcagctct 200  
gatgggatgt gttttccaga gcacagaaga caaatgtata ttcaagatag 250  
actggactct gtcaccagga gagcacgcca aggacgaata tgtgctatac 300  
tattactcca atctcagtgt gcctattggg cgcttccaga accgcgtaca 350  
cttgatgggg gacatcttat gcaatgatgg ctctctcctg ctccaagatg 400  
tgcaagaggc tgaccaggga acctatatct gtgaaatccg cctcaaaggg 450  
gagagccagg tgttcaagaa ggcggtggta ctgcatgtgc ttccagagga 500  
goccaaagag ctcatgggtcc atgtgggtgg attgattcag atgggatgtg 550  
ttttccagag cacagaagtg aaacacgtga ccaaggtaga atggatattt 600  
tcaggacggc gcgcaaagga ggagattgta tttcgttact accacaaact 650  
caggatgtct gtggagtact ccagagctg gggccacttc cagaatcgtg 700  
tgaacctggg gggggacatt ttccgcaatg acggttccat catgcttcaa 750  
ggagtgaggg agtcagatgg aggaaactac acctgcagta tccacctagg 800  
gaacctggtg ttcaagaaaa ccattgtgct gcatgtcagc ccggaagagc 850  
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aatcagttgg tgatcattgt gggaattgtc tgtgccacaa tcctgctgct 950  
ccctgttctg atattgatcg tgaagaagac ctgtggaaat aagagttcag 1000



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tcagatcgga	acaactcact	tgaaaaaaag	tcaggtgggg	gaatgccaaa	1250
aacacagcaa	gccttttgag	aagaatggag	agtcccttca	tctcagcagc	1300
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gaacaggcct	gctgagggga	ggggagcatg	gacttggcct	ctggagtggg	1500
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<211> 394
<212> PRT
<213> Homo sapiens
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				20					25					30
Thr	Val	His	Val	Gly	Asp	Ser	Ala	Leu	Met	Gly	Cys	Val	Phe	Gln
				35					40					45
Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile	Asp	Trp	Thr	Leu	Ser
				50					55					60
Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu	Tyr	Tyr	Tyr	Ser
				65					70					75
Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg	Val	His	Leu
				80					85					90
Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu	Gln	Asp
				95					100					105
Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg	Leu
				110					115					120
Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val
				125					130					135
Leu	Pro	Glu	Glu	Pro	Lys	Glu	Leu	Met	Val	His	Val	Gly	Gly	Leu
				140					145					150
Ile	Gln	Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Val	Lys	His	Val



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 <212> PRT  
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 20 25 30  
 Arg Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val  
 35 40 45  
 Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn  
 50 55 60  
 Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln  
 65 70 75  
 Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu  
 80 85 90  
 Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn  
 95 100 105  
 Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn  
 110 115 120  
 Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala

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Thr Leu Leu Lys	Ile Asp Asn Arg Asn	Ile Val Glu Tyr Ile	Lys		
	140	145	150		
Ala Arg Thr His	Leu Ile Arg Trp Val	Gly Leu Ser Arg Gln	Lys		
	155	160	165		
Ser Asn Glu Val	Trp Lys Trp Glu Asp	Gly Ser Val Ile Ser	Glu		
	170	175	180		
Asn Met Phe Glu	Phe Leu Glu Asp Gly	Lys Gly Asn Met Asn	Cys		
	185	190	195		
Ala Tyr Phe His	Asn Gly Lys Met His	Pro Thr Phe Cys Glu	Asn		
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<220>  
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<210> 427  
 <211> 49  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 427  
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<210> 428  
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<400> 428  
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 <211> 24  
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 <210> 431  
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 <212> DNA  
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 <210> 433  
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 <210> 434  
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 <210> 435  
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 <400> 435  
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 <400> 437  
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<210> 446  
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<210> 458  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 458  
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<210> 459  
<211> 24  
<212> DNA  
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<220>  
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<400> 459  
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<210> 460  
<211> 24  
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<220>  
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<210> 463  
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<210> 494  
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<212> DNA  
<213> Homo Sapien

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<210> 501  
 <211> 640  
 <212> PRT  
 <213> Homo Sapien

<400> 501  
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 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
 35 40 45  
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
 50 55 60  
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
 65 70 75  
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
 80 85 90  
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
 95 100 105  
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
 110 115 120  
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
 125 130 135  
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
 140 145 150  
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser  
 155 160 165





Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro
				485					490					495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr
				500					505					510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr
				515					520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala
				530					535					540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His
				545					550					555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn
				560					565					570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu
				575					580					585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser
				590					595					600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn
				605					610					615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn
				620					625					630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile					
				635					640					

<210> 502  
 <211> 2458  
 <212> DNA  
 <213> Homo Sapien

<400> 502  
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 ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150  
 agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200  
 ccttctctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250  
 ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300  
 caactggggc ttocagaaaa agacactctg gatattgaat ggctgtcac 350  
 cgataatgaa gggaaccaa aagtggatgat cacttactcc agtcgtcatg 400  
 tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450  
 aatttctctg caggagatgc ctccttgag attgaacctc tgaagcccag 500  
 tgatgagggc cggtagacct gtaagggtta gaattcagg cgctacgtgt 550  
 ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccagtggt 600





Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	230	235	240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	245	250	255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	260	265	270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	275	280	285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	290	295	300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	305	310	315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	320	325	330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	335	340	345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	350	355	360
Ser Met Ile Pro	Ser Gln Ser Arg Ala	Phe Gln Thr Val	365	370	

<210> 504  
 <211> 3060  
 <212> DNA  
 <213> Homo Sapien

<400> 504  
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 ccgccgccca cggcacggca gccaccatgg cgctcctgct gtgcttcgtg 100  
 ctctgtgctg gagtagtgga tttcgccaga agtttgagta tcactactcc 150  
 tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgccatgca 200  
 aatttacgct tagtcccgaa gaccagggac cgctggacat cgagtggctg 250  
 atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300  
 tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350  
 attttacgag taatgatctc aaatctggtg atgcatcaat aaatgtaacg 400  
 aatttacaac tgtcagatat tggcacatat cagtgc aaag tgaaaaaagc 450  
 tcctggtgtt gcaaataaga agattcatct ggtagttctt gttaagcctt 500  
 caggtgagat atgttacgtt gatggatctg aagaaattgg aagtgacttt 550  
 aagataaaat gtgaacccaaa agaaggttca cttccattac agtatgagtg 600  
 gcaaaaattg tctgactcac agaaaatgcc cacttcatgg ttagcagaaa 650  
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acatacagct gtacagtcag aaacagagtg ggctctgac agtgcctggt 750  
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ccattatagg aactttgctt gctctagcgc tcattgggtct tatcatcttt 850  
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<210> 505  
<211> 352  
<212> PRT  
<213> Homo Sapien

<400> 505  
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20 25 30  
Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu  
35 40 45  
Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser  
50 55 60  
Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser  
65 70 75  
Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg  
80 85 90  
Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile  
95 100 105  
Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys  
110 115 120  
Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu







<213> Homo Sapien

<400> 507

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Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln  
35 40 45  
Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln  
50 55 60  
Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala  
65 70 75  
Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg  
80 85 90  
Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser  
95 100 105  
Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val  
110 115 120  
Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys  
125 130 135  
Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln  
140 145 150  
Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser  
155 160 165  
Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu  
170 175 180  
Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile  
185 190 195  
Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu  
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<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

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<210> 509

<211> 177

<212> PRT

<213> Homo Sapien

<400> 509

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Ile	Leu	Cys	Ser	Val	Asp	Asn	His	Gly	Leu	Arg	Arg	Cys	Leu	Ile	20	25	30	
Ser	Thr	Asp	Met	His	His	Ile	Glu	Glu	Ser	Phe	Gln	Glu	Ile	Lys	35	40	45	
Arg	Ala	Ile	Gln	Ala	Lys	Asp	Thr	Phe	Pro	Asn	Val	Thr	Ile	Leu	50	55	60	
Ser	Thr	Leu	Glu	Thr	Leu	Gln	Ile	Ile	Lys	Pro	Leu	Asp	Val	Cys	65	70	75	
Cys	Val	Thr	Lys	Asn	Leu	Leu	Ala	Phe	Tyr	Val	Asp	Arg	Val	Phe	80	85	90	
Lys	Asp	His	Gln	Glu	Pro	Asn	Pro	Lys	Ile	Leu	Arg	Lys	Ile	Ser	95	100	105	
Ser	Ile	Ala	Asn	Ser	Phe	Leu	Tyr	Met	Gln	Lys	Thr	Leu	Arg	Gln	110	115	120	
Cys	Gln	Glu	Gln	Arg	Gln	Cys	His	Cys	Arg	Gln	Glu	Ala	Thr	Asn	125	130	135	
Ala	Thr	Arg	Val	Ile	His	Asp	Asn	Tyr	Asp	Gln	Leu	Glu	Val	His	140	145	150	
Ala	Ala	Ala	Ile	Lys	Ser	Leu	Gly	Glu	Leu	Asp	Val	Phe	Leu	Ala				

0959758-41004

155

160

165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala  
170 175

<210> 510

<211> 996

<212> DNA

<213> Homo Sapien

<400> 510

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tccacaggtg tccactccca ggtccaactg cacctcggtt ctatcgataa 200  
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cacaggagct cccgagcgcc gaggacaaca gccgatggc cagtgacca 900  
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<210> 511

<211> 251

<212> PRT

<213> Homo Sapien

<400> 511

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20 25 30

Leu	Leu	Gly	Ser	Ser	Trp	Gly	Gly	Leu	Ile	His	Leu	Tyr	Thr	Ala	
				35					40					45	
Thr	Ala	Arg	Asn	Ser	Tyr	His	Leu	Gln	Ile	His	Lys	Asn	Gly	His	
				50					55					60	
Val	Asp	Gly	Ala	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	
				65					70					75	
Arg	Ser	Glu	Asp	Ala	Gly	Phe	Val	Val	Ile	Thr	Gly	Val	Met	Ser	
				80					85					90	
Arg	Arg	Tyr	Leu	Cys	Met	Asp	Phe	Arg	Gly	Asn	Ile	Phe	Gly	Ser	
				95					100					105	
His	Tyr	Phe	Asp	Pro	Glu	Asn	Cys	Arg	Phe	Gln	His	Gln	Thr	Leu	
				110					115					120	
Glu	Asn	Gly	Tyr	Asp	Val	Tyr	His	Ser	Pro	Gln	Tyr	His	Phe	Leu	
				125					130					135	
Val	Ser	Leu	Gly	Arg	Ala	Lys	Arg	Ala	Phe	Leu	Pro	Gly	Met	Asn	
				140					145					150	
Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	Ser	Arg	Arg	Asn	Glu	Ile	Pro	
				155					160					165	
Leu	Ile	His	Phe	Asn	Thr	Pro	Ile	Pro	Arg	Arg	His	Thr	Arg	Ser	
				170					175					180	
Ala	Glu	Asp	Asp	Ser	Glu	Arg	Asp	Pro	Leu	Asn	Val	Leu	Lys	Pro	
				185					190					195	
Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	Ser	Gln	Glu	Leu	
				200					205					210	
Pro	Ser	Ala	Glu	Asp	Asn	Ser	Pro	Met	Ala	Ser	Asp	Pro	Leu	Gly	
				215					220					225	
Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	Thr	Gly	
				230					235					240	
Pro	Glu	Gly	Cys	Arg	Pro	Phe	Ala	Lys	Phe	Ile					
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 <211> 2015  
 <212> DNA  
 <213> Homo Sapien

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 ctgctgggag gttggggtct ctgggagctc tgcaggcccc agcaccgcga 150  
 gagcagacac tgcgatgaca acggacgaca cagaagtgcc cgctatgact 200  
 ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250  
 ctcttctagg gcctcaaccc cagccggccc cattccagaa gcagagacca 300

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 cgccagtggc agccccgagg gagctggaat gaccacagtt cagaccatca 450  
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 catccctggg gcctcagaca tagatctcat cccacaggaa ggggtgaagg 900  
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 ctaacagcgc cacagaaaga gaagtgcag caccgggggc cagaccctc 1100  
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 gtggcccaaa aaaaa 2015

<210> 513  
 <211> 482  
 <212> PRT  
 <213> Homo Sapien

<400> 513  
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 35 40 45  
 Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu  
 50 55 60  
 Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile  
 65 70 75  
 Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg  
 80 85 90  
 Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu  
 95 100 105  
 Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu  
 110 115 120  
 Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro  
 125 130 135  
 Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu  
 140 145 150  
 Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr  
 155 160 165  
 Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser  
 170 175 180  
 Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser  
 185 190 195  
 Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg  
 200 205 210  
 Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile  
 215 220 225  
 Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu  
 230 235 240  
 Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile  
 245 250 255

Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	260	265	270
Ile	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	275	280	285
Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	290	295	300
Thr	Glu	Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	305	310	315
Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	320	325	330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	335	340	345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	350	355	360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	365	370	375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	380	385	390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro	395	400	405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr	410	415	420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro	425	430	435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr	440	445	450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met	455	460	465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro	470	475	480

Gln Thr

<210> 514

<211> 2284

<212> DNA

<213> Homo Sapien

<400> 514

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gacaaaaact aaactgaaat ttaaaatggt cttcggggga gaaggagct 250

tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300  
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 gtcattctctt tctaagggaa tcagaggcaa tgagcccgtataatacttcaa 400  
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 acacctgggt gatTTTTTgta ttttttagtag agacgggggt tcacatggt 1850



Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	21.5%
Education (years)	Mean (SD)
Male	12.5 (2.1)
Female	11.8 (2.5)
Occupation	
Professional	35.2%
Managerial	28.7%
Skilled	15.3%
Unskilled	20.8%
Income (USD/month)	Mean (SD)
Male	1,250 (350)
Female	1,180 (320)
Health insurance	
Yes	92.1%
No	7.9%

<400>	515													
Met	Phe	Phe	Gly	Gly	Glu	Gly	Ser	Leu	Thr	Tyr	Thr	Leu	Val	Ile
1				5					10					15
Ile	Cys	Phe	Leu	Thr	Leu	Arg	Leu	Ser	Ala	Ser	Gln	Asn	Cys	Leu
				20					25					30
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu
				35					40					45
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln
				50					55					60
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly
				65					70					75
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala
				80					85					90
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala
				95					100					105
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile
				110					115					120
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu
				125					130					135
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val
				140					145					150
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp
				155					160					165
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp
				170					175					180
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu
				185					190					195

Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser	
				200					205					210	
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala	
				215					220					225	
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala	
				230					235					240	
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr	
				245					250					255	
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro	
				260					265					270	
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr	
				275					280					285	
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr	
				290					295					300	
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly	
				305					310					315	
Ser	Leu	Glu	Thr	Ile	Pro	Phe	Thr	Glu	Ile	Ser	Asn	Leu	Thr	Leu	
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Asn	Thr	Gly	Asn	Val	Tyr	Asn	Pro	Thr	Ala	Leu	Ser	Met	Ser	Asn	
				335					340					345	
Val	Glu	Ser	Ser	Thr	Met	Asn	Lys	Thr	Ala	Ser	Trp	Glu	Gly	Arg	
				350					355					360	
Glu	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Gln	Gly	Ser	Val	Pro	Glu	Asn	
				365					370					375	
Gln	Tyr	Gly	Leu	Pro	Phe	Glu	Lys	Trp	Leu	Leu	Ile	Gly	Ser	Leu	
				380					385					390	
Leu	Phe	Gly	Val	Leu	Phe	Leu	Val	Ile	Gly	Leu	Val	Leu	Leu	Gly	
				395					400					405	
Arg	Ile	Leu	Ser	Glu	Ser	Leu	Arg	Arg	Lys	Arg	Tyr	Ser	Arg	Leu	
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Asp	Tyr	Leu	Ile	Asn	Gly	Ile	Tyr	Val	Asp	Ile					
				425					430						

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 <213> Homo Sapien

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 <222> 1869, 1887  
 <223> unknown base

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cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400  
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Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120
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Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150
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Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195
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Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	230	235	240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	245	250	255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	260	265	270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	275	280	285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	290	295	300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	305	310	315
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Figure 1. The effect of the concentration of the *Agrobacterium* strain on the transformation efficiency of *Agrobacterium* strain 104. The concentration of the *Agrobacterium* strain 104 was varied from 10<sup>6</sup> to 10<sup>9</sup> cells/ml. The transformation efficiency was determined by the number of transformants per 10<sup>6</sup> cells of the *Agrobacterium* strain 104. The data are the mean  $\pm$  SD of three independent experiments. The transformation efficiency was significantly higher at 10<sup>8</sup> cells/ml than at 10<sup>6</sup> and 10<sup>7</sup> cells/ml ( $P < 0.05$ ).

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<400> 519

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<220>

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